

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

COSEY
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:14:56 ; Search time 97.0088 Seconds
(without alignments)
1374.564 Million cell updates/sec

Title: US-09-811-367b-1
Perfect score: 1023
Sequence: 1 MTDSVIYSMLPLTATOQN.....GLQASSCEVPLHGCKKAVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 9256

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	100.0	189	2	043198_HUMAN
2	1007	98.4	189	2	075613_HUMAN
3	548.5	53.6	188	2	088713_MOUSE
4	525.5	51.4	188	2	064335_RAT
5	170.5	16.7	188	2	062YP6_CHICK
6	168.5	16.5	188	2	062YP3_CHICK
7	159	15.5	188	1	CLCSA_HUMAN
8	159	15.5	188	1	052M11_HUMAN
9	131.5	12.9	189	2	08C634_MOUSE
10	126	12.3	189	2	061969_MOUSE
11	106.5	10.4	189	2	096DB9_HUMAN
12	103.5	10.1	188	2	09W012_DROME
13	96.5	9.4	189	2	060S03_CAEBR
14	92.5	9.0	188	2	09T275_CAEBL
15	82.5	8.1	189	2	018202_CAEBL
16	72.5	7.1	188	2	09W108_DROME
17	69	6.7	189	2	09MF32_SCUCU
18	67	6.5	189	2	09MF30_SCUCU
19	66.5	6.5	188	2	07K7K8_CAEBL
20	65.5	6.4	189	2	086129_MYTEL
21	60.5	5.9	188	2	0814K8_CAEBL
22	60.5	5.9	189	2	07PL10_DROME
23	58	5.7	188	2	030134_ARCTU
24	58	5.7	189	2	023831_PCRYT
25	58	5.7	189	2	075J03_DICDI
26	57.5	5.6	188	2	04UHL7_THEAN
27	57	5.6	188	2	028946_PIG
28	57	5.6	188	2	06MK93_BDEBA
29	57	5.6	189	2	08W0R0_3CRYT
30	56	5.5	189	2	08W0S9_CHICK
31	55.5	5.4	188	1	V060_F0WPFV

32	55.5	5.4	188	2	06UDX7_9DIPR	061dx7 cuterebra f
33	55.5	5.4	188	2	070H91_F0WPFV	070h91 fowlpox vir
34	55.5	5.4	188	2	04SYA7_TETNG	04syat tetraxod n
35	55.5	5.4	189	2	06ZRB9_HUMAN	06zrb9 homo sapien
36	55.5	5.4	189	2	09XXB7_CAEBL	09xxb7 caenorhabd
37	55.5	5.4	189	2	04RSS5_TETNG	04rss5 tetraxod n
38	55.5	5.4	188	2	054V41_DICDI	054v41 dictyostell
39	55.5	5.4	188	2	068P15_CENSC	068p15 centruroid
40	55.5	5.4	188	2	04YFS2_PLABE	04yfs2 plasmodium
41	55.5	5.4	188	2	05N2Z9_ACOSE	05n2z9 azaricus sp
42	54.5	5.3	189	1	E321_ADB07	P15138 human adeno
43	54.5	5.3	189	2	05MD81_9DIPR	05md81 diplochora
44	54.5	5.3	189	2	09PE95_XYLEFA	09pe95 xyella fas
45	54.5	5.3	189	2	05EY51_ADB07	05ey51 human adeno

ALIGNMENTS

RESULT 1	043198_HUMAN	PRELIMINARY;	PRT;	189 AA.
ID	043198_HUMAN	PRELIMINARY;	PRT;	189 AA.
AC	043198;			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Maat cell function-associated antigen.			
GN	Name=MAFA;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Enzyme digested lung;			
RX	MEDLINE=98438735, PubMed=9765598; DOI=10.1016/S0167-4781(98)00107-9;			
RA	Lamers M.B., Lamont A.G., Williams D.H.;			
RT	"Human MAFa has alternatively spliced variants."			
RL	Biochim. Biophys. Acta 1399:209-212 (1998).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Enzyme digested lung;			
RA	Lamers M.B.A.C., Lamont A.G., Williams D.H.;			
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF034952; AAC34731.1; -; mRNA.			
DR	HSSP; O13241; 1B6E.			
DR	GO; GO:0016021; C:integral to membrane; TAS.			
DR	GO; GO:0004872; F:receptor activity; TAS.			
DR	GO; GO:0005229; F:sugar binding; TAS.			
DR	GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.			
DR	GO; GO:0006968; P:cellular defense response; TAS.			
DR	GO; GO:0006954; P:inflammatory response; TAS.			
DR	InterPro: IPR001304; Lectin_C.			
DR	Pfam: PF00059; Lectin_C_1.			
DR	SMART; SM00034; CUECT_1.			
DR	PROSITE; PSS0041; C-TYPE_LECTIN_2, 1.			
DR	SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;			
QY	Query Match	100.0%;	Score 1023;	DB 2; Length 189;
QY	Best Local Similarity	100.0%;	Pred. No. 2, 7e-89;	
QY	Matches 189;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MTDSVIYSMLPLTATOQNNDYGPQKSSSKPSCGLVATITGLTAVLLSVLLYMWL	60	
QY	1	MTDSVIYSMLPLTATOQNNDYGPQKSSSKPSCGLVATITGLTAVLLSVLLYMWL	60	
QY	61	COGSNSTCASGSCPDPMKYGKHCYFSEVERKDMNSLEFCLARDSHLLVTTDQEMS	120	
QY	61	COGSNSTCASGSCPDPMKYGKHCYFSEVERKDMNSLEFCLARDSHLLVTTDQEMS	120	
QY	121	LLOVYFSEARFCWIGLRNNSGMRWEDGSLNFSRISNSFVOTGALINKGLQASSCEVPL	180	
QY	121	LLOVYFSEARFCWIGLRNNSGMRWEDGSLNFSRISNSFVOTGALINKGLQASSCEVPL	180	

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Db      121 LLQVFLSEAFQWIGLNNNGWMEWDSPLNFSRISNSFVQTCAINKGLQASSCEVPL 180
Qy      181 HGVCKKVR 189
Db      181 HGVCKKVR 189

RESULT 2
075613 HUMAN PRELIMINARY; PRT; 189 AA.
ID      075613
AC      075613
DT      01-NOV-1998 (TrEMBLrel. 08, Created)
DT      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT      01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE      ITIM-containing receptor MAFR-L (mast cell function-associated antigen
DE      homolog).
GN      Name=MAFR;
OS      Homo sapiens (Human).
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Homo
NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=99057052; PubMed=9842918;
RX      DOI=10.1002/(SICI)1521-4141(199811)28:11<3755::AID-IMMU3755>3.0.CO;2-3;
RA      Butcher S., Arney K.L., Cook G.P.;
RT      "MAFR-L, an ITIM-containing receptor encoded by the human NK cell gene
RT      complex and expressed by basophils and NK cells.";
RL      Eur. J. Immunol. 28:3755-3762(1998).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=99077194; PubMed=9862378;
RA      Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT      "2F1 antigen, the mouse homolog of the rat 'mast cell function-
RT      associated antigen', is a lectin-like type II transmembrane receptor
RT      expressed by natural killer cells.";
RL      Eur. J. Immunol. 28:4409-4417(1998).
DR      EMBL; AF081675; AAC3200.1; -; mRNA.
DR      EMBL; AF097358; AAD03719.1; -; mRNA.
DR      HSSP; Q13241; 1B6E.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0005529; F:sugar binding; IEA.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; Lectin_C.1.
DR      SMART; SM00034; CLECT_1.
DR      PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW      Receptor.
SQ      SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

Query Match      98.4%; Score 1007; DB 2; Length 189;
Best Local Similarity 98.4%; Pred. No. 9, 2e-88;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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ID      088713 MOUSE PRELIMINARY; PRT; 188 AA.
AC      088713
DT      01-NOV-1998 (TrEMBLrel. 08, Created)
DT      01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT      10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE      Mast cell function-associated antigen 2F1 (killer cell lectin-like
DE      receptor G1) (MAFA).
GN      Name=Klrg1; Synonyms=MAfa, mafa;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C.B-17 SCID;
RX      MEDLINE=99077194; PubMed=9862378;
RA      Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT      "2F1 antigen, the mouse homolog of the rat 'mast cell function-
RT      associated antigen', is a lectin-like type II transmembrane receptor
RT      expressed by natural killer cells.";
RL      Eur. J. Immunol. 28:4409-4417(1998).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=129/SvevTACFB; TISSUE=Spleen;
RX      MEDLINE=21115136; PubMed=1120622; DOI=10.1007/s002510000282;
RA      Voeltinger D., Kaufmann M., Pircher H.;
RT      "Genomic structure, alternative splicing, and physical mapping of the
RT      killer cell lectin-like receptor G1 gene (Klrg1), the mouse homologue
RT      of MAFR.";
RL      Immunogenetics 52:206-211(2001).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=99077501; PubMed=9862665;
RA      Blaser C., Kaufmann M., Pircher H.;
RT      "Virus-activated CD8 T cells and lymphokine-activated NK cells express
RT      the mast cell function-associated antigen MAFA, an inhibitory C-type
RT      lectin.";
RL      J. Immunol. 161:6451-6454(1998).
DR      EMBL; AF097357; AAD03718.1; -; mRNA.
DR      EMBL; AF317727; AAK40082.1; -; Genomic DNA.
DR      EMBL; AJ010751; CAA09342.1; -; mRNA.
DR      HSSP; Q13241; 1B6E.
DR      Ensemble; ENSMUSG0000030114; Mus musculus.
DR      MGI; MGI:1355294; Klrg1.
DR      GO; GO:0016021; C:integral to membrane; TAS.
DR      GO; GO:0005529; F:sugar binding; TAS.
DR      GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR      InterPro; IPR001304; Lectin_C.
DR      Pfam; PF00059; Lectin_C.1.
DR      SMART; SM00034; CLECT_1.
DR      PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW      Lectin; Receptor.
FT      CHAIN 2 188 mast cell function-associated antigen
FT      (MAFA).
SQ      SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;

Query Match      53.6%; Score 548.5; DB 2; Length 188;
Best Local Similarity 55.6%; Pred. No. 4, 5e-44;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
```

RESULT 3
088713_MOUSE

QY 181 HGVCCKV 187
ID :|||
DB 180 QWICKKV 186

RESULT 4

064335_RAT PRELIMINARY; PRT; 188 AA.

AC 064335;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, last annotation update)
GN MAFa protein (Mast cell) function associated antigen.
DN Name=Klrl1; Synonyms=MAFA, mafa;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague Dawley; TISSUE=Testis;
RX MEDLINE=97240766; PubMed=9120279;
RA Bocek U P., Gutmann M.D., Pecht I.;
RT "Analysis of the gene encoding the mast cell function-associated
RT antigen and its alternatively spliced transcripts."
RL J. Immunol. 158:3235-3243(1997).
[2]
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96016176; PubMed=7568140;
RA Gutmann M.D., Tai M., Pecht I.;
RT "A secretion inhibitory signal transduction molecule on mast cells is
RT another C-type lectin."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97193; CAAG5829.1; -; Genomic_DNA.
DR EMBL; X79812; CAAG6208.1; -; mRNA.
DR EMBL; X79812; CAAG6208.1; -; mRNA.
DR EMBL; X97193; CAAG5829.1; JOINED; Genomic_DNA.
DR EMBL; X97193; CAAG5829.1; JOINED; Genomic_DNA.
DR EMBL; X97194; CAAG5829.1; JOINED; Genomic_DNA.
DR EMBL; X97195; CAAG5829.1; JOINED; Genomic_DNA.
DR PIR; I59421; I59421.
DR HSSP; P26718; IKCG.
DR Ensembl; ENSRNOG0000014918; Rattus norvegicus.
DR RGD; 61978; Klrl1.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 188 AA; 21356 MW; 3CC08032D4D020B15 CRC64;

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 6.9e-42; Indels 1; Gaps 1;
Matches 100; Conservative 29; Mismatches 57;

QY 1 MTDSVISMELPTATQANDYGFQKSSSSKSPSCCLVAITLGLTAVLLSVLYQMIL 60
DB 1 MAONSTISTLELPAARVPQDSDRWKAVVLRPCVSLVWVAGLTVILMSLLVYQRTL 60
QY 61 CCGSNSTSCASCPCSPDRMKYGNHCYFVSVEEDKNNSLFELCLARSHLVTINDNEMS 120
DB 61 CCGSKGFMCSQCSFPLMMRNNGSHCYFVSWEKRDNNSLKFCADKSHLITPPDNGVN 120
QY 121 LLDVFLSEAFQWGLRNNSGMRWEDGSLNPSRISNSPVOTGATKNGLOASCEVPL 180
DB 121 LFDYVEDEDFYWGRLRIDGMRWEDGSLNPSRISNSPVOTGATKNGLOASCEVAL 179

QY 181 HGVCCKV 187
ID :|||
DB 180 QWICKKV 186

RESULT 5

06ZYP6_CHICK PRELIMINARY; PRT; 188 AA.

AC 06ZYP6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)
DE B-1ec protein.
GN Name=B-1ec;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RX PubMed=15749883;
RA Rogers S.L., Gobel T.W., Vierterboeck B.C., Milne S., Beck S.,
RA Kaufman J.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT reveals that the NK Complex and the MHC share a common ancestral
RT region."
RL J. Immunol. 174:3475-3483(2005).
[2]
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RA Rogers S.L.;
RT "Characterisation of C-type lectin-like receptors in the chicken
RT MHC."
RL Thesis (2002), Department of Pathology and Microbiology, University of
RL Bristol, Bristol, United Kingdom.
[3]
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bone marrow;
RA Kaufman J.F.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ614334; CAG25418.1; -; mRNA.
DR HSSP; Q9H8F0; 1K9J.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZE2II.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 188 AA; 20997 MW; 9FDB5BD2D9BF9FE41 CRC64;

Query Match 16.7%; Score 170.5; DB 2; Length 188;
Best Local Similarity 27.3%; Pred. No. 4.7e-08; Indels 27; Gaps 6;
Matches 48; Conservative 24; Mismatches 77;

QY 26 QKSSSSKSPSC-----SCLVAITLGLTAVLLSVLYQMILCOGSNSTCASCPCSPDRM 80
DB 17 RREGPSRGACVTFQULMAAIFVLLITAVAFNAOAO-----PHQPCACQCPDWM 67
QY 81 KYGNHCYFVSVEEDKNNSLFELCLARSHLVTINDNEMSLLVFLSEAFQWGLRNN 139
DB 68 GFRGKCYCYFSEDESNNTSSQNNCSALGASIAVFPDSEADISFTMRKHGSSPHWVGLSREGK 127
QY 140 --GWRWEDGSLNPSRISNSF--VQ--TCGATKNGLOASCEVPLHGVCCKVRL 189
DB 128 EHAMEWVNRSPPL-----SHLFDVQGDGLCAVYLDAGLSSSHCSARRRWVCTYRPL 177

RESULT 6

06ZYP3_CHICK PRELIMINARY; PRT; 188 AA.

AC 06ZYP3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)
DE B-1ec protein.

```

GN Name=B-1ec;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RX PubMed=1579883;
RA Rogers S.L., Gobel T.W., Viertlboeck B.C., Milne S., Beck S.,
RA Kaufman J.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT reveals that the NK Complex and the MHC share a common ancestral
RT region.";
RL J. Immunol. 174:3475-3483 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RA Rogers S.L.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT reveals that the NK Complex and the MHC share a common ancestral
RT region.";
RL J. Immunol. 174:3475-3483 (2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RA Rogers S.L.;
RT "Characterisation of C-type lectin-like receptors in the chicken
RT MHC.";
RL Thesis (2002), Department of Pathology and Microbiology, University of
RL Bristol, Bristol, United Kingdom.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RA Kaufman J.F.;
RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ634337; CAG25421.1; -; mRNA.
DR HSP; O9H8F0; 1K99.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; Antifreeze2.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTI-FREEZE1.
DR SMART; SM00354; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN_1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 188 AA; 21053 MW; 6AD5AC9CB8F440 CRC64;

Query Match 16.5%; Score 168.5; DB 2; Length 188;
Best Local Similarity 27.3%; Pred. No. 7.3e-08;
Matches 48; Conservative 24; Mismatches 77; Indels 27; Gaps 6;

QY 26 QSSSSSKPSC-----SCLVAITLGLTAVLSVLVLYQWILCGSNYSTCAGSPCPDRM 80
DB 17 RREGPSRACVTFQLTMAVFTVLLITVAFAVQAFQ-----PHPOCAQCPDWI 67
QY 81 KYGNHCYFVSVEEKDWNSSLEFCIARDSHLVITDQEMSLIQVLEAFICIGLRNNS- 139
DB 68 GRGKCYFVSDEBSNWTSSQNNCSALGASLAFDSDSDSPMRKKGSPHVGSLRBEK 127

QY 140 --GWRWEDGSPINFRISNSF-VQ--TCGAINKNGIQAASSCEVPLHGVCXKRL 189
DB 128 EHPMEWVNSPL-----SHLFQVQDGLCAVILGADGLSSSHCSRMRMVCXKPL 177

RESULT 7
ID CLC5A HUMAN STANDARD; PRT; 188 AA.
AC Q9NY25; O9UK00;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE C-type lectin domain family 5 member A (C-type lectin superfamily
DE member 5) (Myeloid DAP12-associating lectin) (MDL-1).
GN Name=CLC5A; Synonyms=CLEC5F5, MDL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2), FUNCTION, TISSUE SPECIFICITY,
RP INTERACTION WITH TYROBP, AND MUTAGENESIS OF LYS-16.
RX MEDLINE=99380598; PubMed=10449773; DOI=10.1073/pnas.96.17.9792;
RA Baker A.B.H., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.,
RA "Myeloid DAP12-associating lectin (MDL)-1 is a cell surface receptor
RT involved in the activation of myeloid cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RA Mueller A., Metz H., Feller A.C.;
RT "Expression of MDL-1 in human blood and cell lines.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delahunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vandrunft A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozerky P., Bielicki L., Scott K., Holmes A., Harting R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Stromatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Moesner J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Speith J.,
RA Bieri T.A., Nelson J.O., Berkowitz N., Wohlmann P.E., Cook L.L.,
RA Hickendolham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Zhou Y., James R., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadonoto S., Bubb E.,
RA Sims E., Levy R., Clendenning J., Kaul R., Kent W.J., Frey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164 (2003).
CC -!- FUNCTION: May be involved in proinflammatory activation of myeloid
CC cells via TYROBP-mediated signaling in a calcium-dependent manner.
CC -!- SUBUNIT: Interacts with TYROBP.
CC -!- TISSUE SPECIFICITY: Expressed in peripheral blood monocytes and in
CC the monocyte/macrophage cell lines U937 and MonoMac6, but not in
CC cell lines of other origins. Expression is down-regulated when
CC monocytes differentiate into dendritic cells.
CC -!- SIMILARITY: Contains 1 C-type lectin domain.
CC This Swiss-Prot entry is copy-right. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL: AF139768; AAF02491.1; -; mRNA.
CC EMBL: AJ271684; CAB71334.1; -; mRNA.
CC EMBL: AC073647; AAS07444.1; -; Genomic_DNA.
CC HSSP: P22897; IE63.
CC Ensembl: ENSG00000090269; Homo sapiens.
CC HGNC: HGNC:2054; CLC5A.
CC MIM: 604987; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005488; F:binding; TAS.
CC GO; GO:0006968; P:cellular defense response; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR002353; Antifreeze2.

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DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PRO00356; ANTI_FERREZII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS00641; C_TYPE_LECTIN_2; 1.
DR Alternative splicing; Glycoprotein; Immune response; Lectin;
KW Signal-anchor; Transmembrane.
FT TOPO_DOM 1 4 Cytoplasmic (Potential).
FT TRANSMEM 5 27 Signal-anchor for type II membrane
FT 78 188 protein (Potential).
FT DOMAIN 78 188 Extracellular (Potential).
FT CARBOHYD 32 32 C-type lectin.
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
FT DISULFID 71 82 By similarity.
FT DISULFID 99 183 By similarity.
FT DISULFID 161 175 By similarity.
FT VARSPLIC 116 116 Missing (in isoform 2).
FT MUTAGEN 16 16 K->I: Abolishes interaction with TYROBP.
SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;
Query Match 15.5%; Score 159; DB 1; Length 188;
Best Local Similarity 26.5%; Pred. No. 5.8e-07;
Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;
QY 41 ITLGLTAVLSV-----LLYQWILCOGSN-----YSTC-----ASCPS----- 74
DB 6 IISGLIVLVKRVGMTLFLYFPQIFNKSNDGFTTTRSGYTSQIRGSSSPSPNGFITTR 65
QY 75 -----CPDRMKYGNHCYFVSVEKDMNSLFCILARDSHLVITDNOEMLQVFLSEA 129
DB 66 SYGTVCPKMEFYQARCFPLSTSSSWNSRDFCKGKSTLAVTPPEKLFQDITDAE 125
QY 130 FCWIGL---RNNSGMWEDGSPINFRISNSFVOTCGAIN-KNGIQASSCEVPLHGVC 185
DB 126 KYFICGLIYHREKRWKRNINSVFN-GNVTNQNQNFNCATIGLKTPTDASCDISYRICE 184
QY 186 K 186
DB 185 K 185
RESULT 8
Q52M11 HUMAN PRELIMINARY; PRT; 188 AA.
ID -Q52M11 HUMAN PRELIMINARY; PRT; 188 AA.
AC Q52M11;
DT 11-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 11-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE C-type lectin, superfamily member 5.
GN Name=CLECTA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=lung and heart;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Tohtiyuki S., Carninci P., Prange S.,
RA Raha S.S., Loquellano N.A., Peters G.J., Aramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung and heart;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC093714; AAH93714.1; -; mRNA.
KW Lectin.
SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;
Query Match 15.5%; Score 159; DB 2; Length 188;
Best Local Similarity 26.5%; Pred. No. 5.8e-07;
Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;
QY 41 ITLGLTAVLSV-----LLYQWILCOGSN-----YSTC-----ASCPS----- 74
DB 6 IISGLIVLVKRVGMTLFLYFPQIFNKSNDGFTTTRSGYTSQIRGSSSPSPNGFITTR 65
QY 75 -----CPDRMKYGNHCYFVSVEKDMNSLFCILARDSHLVITDNOEMLQVFLSEA 129
DB 66 SYGTVCPKMEFYQARCFPLSTSSSWNSRDFCKGKSTLAVTPPEKLFQDITDAE 125
QY 130 FCWIGL---RNNSGMWEDGSPINFRISNSFVOTCGAIN-KNGIQASSCEVPLHGVC 185
DB 126 KYFICGLIYHREKRWKRNINSVFN-GNVTNQNQNFNCATIGLKTPTDASCDISYRICE 184
QY 186 K 186
DB 185 K 185
RESULT 9
Q8C634 MOUSE
ID Q8C634 MOUSE PRELIMINARY; PRT; 189 AA.
AC Q8C634;
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4922502D1 product:hypothetical C-type lectin domain
DE containing protein, full insert sequence (Similar to C lectin-related
DE protein A).
GN Name=4922502D21Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arai T., Hara A., Fukunishi Y., Komori H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Giesi C., King B., Kooch H.,
 RA Kuehl P., Lewis S., Mateo Y., Nikiel D., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Oxford J., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehama J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsunki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Aichi J., Bono H., Kondo S.,
 RA Nikiel D., Oatso N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Quackenbush J.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grimmond S., Guernicich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kari A., Kawai H., Kawasawa Y., Kedler R.M., Kling B.L.,
 RA Kongsava A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
 RA Maglott D.R., Marchionni L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Seton M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Wanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagasaki T., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunari T., Taehiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Hatada K.,
 RA Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "Riken integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 [6]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Aichi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Katsunari T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsumura T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito K., Saitoh H., Sakai K., Sakazume N., Sano H.,
 RA Sato R., Saitoh H., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shingawa A., Shitaki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscati T.B., Toshitsugu S., Carninci P., Mullane C.,
 RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Prillaby S.J.,
 RA Boeck S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,
 RA Scherch A., Schin J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis.
 RA DIRECTOR MGC Project;
 RL Submitted (Feb-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK076635; BAC36425.1; -; mRNA.
 DR EMBL; BC089479; AAH89479.1; -; mRNA.
 DR Ensembl; ENSMUSG0000047720; Mus musculus.
 DR MGI; MGI:2685920; 4922502D21Rik.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C_1.
 DR SMART; SMO0034; CLECT_1.
 DR PROSITE; PS50041; C-type LECTIN_2; 1.
 KW Hypothetical protein, lectin.
 SQ SEQUENCE 189 AA; 22107 MW; 2EE5673DBACB239E CRC64;
 Query Match 12.9%; Score 131.5; DB 2; Length 189;
 Best Local Similarity 24.2%; Pred. NO.0.00024;
 Matches 45; Conservative 34; Mismatches 86; Indels 21; Gaps 8;
 QY 19 QNDGPGQKSSSSKPSGSCIV-----AITGLLTVLVLSTLY-----OMILQGSNY 66
 DB 2 QDTPSPRLPQTSHERHRLMFDAAKVTLLTLLGAAVAVALWGFSPPRKTVTRARN 61
 QY 67 STC-ASCSPCDRWKYNKNCYFVSEBKDNSSLEFLARDSHLYTTDNGEMSLQVF 125
 DB 62 KTCDDVEVLCPEDWVKLRQNCFSRIQHNKSWLTANDTELDATLAIVTIDTEVEILMNQ 121
 QY 126 LSE-AFCWIGD--RNNSG-WRMEDGSPL-NFSRISSSNGFVOTCCAGINKNGLOASSCEVPL 180
 DB 122 IOEMKTYIIGLHRQNLGILWWTNOSKYNLHEIODHG---QCAFVHQKGLDSTSCEDQK 178
 QY 181 HGVCKK 186
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QY 11 ELPTATQANDYG-PQKSSSKPSCSCVATLTGLTAVLSVLVYLQWILCO-GSNYST 68
DB 35 EEP--TQLONFEGRTETETIRLREKVERLEKLVG-----LQSLMKENNTTESGSKR- 86
QY 69 CASCSCEPDRMMKYGHCYFVSEKDNSSLFCLARDSHLLVITDNOE-----MSLIQ 123
DB 87 -----FFBERKQWDAERHCQGFAGHLAII-DNEAKNTPVTNLIN 125
QY 124 VFLSEAFWIGLRNNSGWMEDGSPINFSRISNSFVOTCGAINKNGL-QASSCEVPLHG 182
DB 126 SSETSDFAWIGMKTKTS--TQTSTP--FTNPDSESPIDGCAVVDKGVMSIRSCIQLRPF 181
QY 183 VCKKVR 188
DB 182 VCOIIR 187

RESULT 14
Q9T275_CAEEL PRELIMINARY; PRT; 188 AA.
AC Q9T275;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein F40G9.10.
GN ORFNames=F40G9.10;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Ploiderinae; Caenorhabditis.
OC NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2; PubMed=9851916;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AF099919; AAC68804.1; -; Genomic_DNA.
DR PIR; T33623; T33623.
DR HSSP; P22897; 1EGG.
DR Ensembl; F40G9.10; Caenorhabditis elegans.
DR WormBase; WBGene00018246; F40G9.10.
DR WormPep; F40G9.10; CE19857.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 188 AA; 21382 MW; CFAC99FAB3032547 CRC64;

Query Match 9.0%; Score 92.5; DB 2; Length 188;
Best Local Similarity 31.4%; Pred. No. 1.3;
Matches 27; Conservative 10; Mismatches 32; Indels 17; Gaps 4;

QY 79 WMKYGNHCYFVSEKDNSSLFCLARDSHLLVI---TDNQMSLIQVFLSEA----- 129
DB 54 WFSYTFICYSTARANFNANACRSESESLASIHSTENQFL---VQLSAAGRVNS 109
QY 130 ---FCWIGL-RNNSGWMEDGSPIN 151
DB 110 KTVYVMIGLIFENREWSMTDSSVNY 135

RESULT 15
Q18202_CAEEL PRELIMINARY; PRT; 189 AA.
AC Q18202;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein Y48E1B.9.

```

```

GN ORFNames=Y48E1B.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Ploiderinae; Caenorhabditis.
OC NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2; PubMed=9851916;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z83383; CAB07697.2; -; Genomic_DNA.
DR PIR; T27020; T27020.
DR HSSP; P22030; 1FVU.
DR Ensembl; Y48E1B.9; Caenorhabditis elegans.
DR WormBase; WBGene00013008; Y48E1B.9.
DR WormPep; Y48E1B.9; CE36239.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 189 AA; 21548 MW; 192DA964586072F0 CRC64;

Query Match 8.1%; Score 82.5; DB 2; Length 189;
Best Local Similarity 22.6%; Pred. No. 11;
Matches 42; Conservative 30; Mismatches 73; Indels 41; Gaps 10;

QY 11 ELPTATQANDYG-PQKSSSKPSCSCVATLTGLTAVLSVLVYLQWILCO-GSNYST 68
DB 32 EEP--TQLONFEGRTETETIRLREKVARLEKLIDG-----LQSLMKENNTTESGSKR- 83
QY 69 CASCSCEPDRMMKYGHCYFVSEKDNSSLFCLARDSHLLVITDNOE-----MSLIQ 123
DB 84 -----LFEERKSWDAERHCQGFAGHLAII-DNEAKNTPVTNLIN 122
QY 124 VFLSEAFWIGLRNNSGWMEDGSPINFSRISNSFVOTCGAINKNGL-QASSCEVPLHG 182
DB 123 SSETSDFAWIGMKTKT--TTQTSTP--FTNPDSESPIDGCAVVDKGVMSIRSCIQLRPF 178
QY 183 VCKKVR 188
DB 179 VCOIIR 184

Search completed: January 9, 2006, 15:35:26
Job time: 100.009 secs

```

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OW protein - protein search, using SW model

Run on: January 9, 2006, 15:16:01 ; Search time 18.3962 Seconds
(without alignment)
988,409 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDVSVIYSMLLPATQAQN.....GLQASSCEVPLHGVCCKVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1164

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	525.5	51.4	188	2	I59421	mast cell function
2	92.5	9.0	188	2	T33623	hypothetical prote
3	5.7	188	2	F69262	hypothetical prote	
4	55.5	5.4	189	2	T27306	hypothetical prote
5	55	5.4	188	2	A39185	virulence protein
6	55	5.4	189	2	T19559	hypothetical prote
7	54.5	5.3	189	1	ERAD75	early E3 20.6k gly
8	54.5	5.3	189	2	D82719	tryptophan repress
9	52	5.1	189	1	JC5394	DJ-1 protein - hum
10	49.5	4.8	189	1	ERAD35	early E3 20.5k gly
11	49.5	4.8	189	2	SS2803	hypothetical prote
12	49.5	4.8	189	2	AE1446	probable scaffold
13	48.5	4.7	189	2	AH3634	core protein [impo
14	48	4.7	188	2	AC1355	methylphosphotries
15	48	4.7	188	2	H90106	60S ribosomal prot
16	48	4.7	189	2	AG1947	hypothetical prote
17	47.5	4.6	189	2	S78046	ribonuclease 6 (EC
18	47	4.6	189	1	IYHUF	interferon alpha-I
19	47	4.6	189	2	I84464	interferon-alpha-F
20	47	4.6	189	2	AD3015	conserved hypotet
21	47	4.6	189	2	C98269	probable general s
22	46	4.5	188	2	JC6547	high sulfur protei
23	46	4.5	189	2	DB1564	hypothetical prote
24	45.5	4.4	188	2	G75326	probable 16S rRNA
25	45	4.4	189	2	S34632	dnab protein homol
26	44.5	4.3	188	2	T17574	hypothetical prote
27	44	4.3	189	2	A25556	hypothetical 21.2K
28	44	4.3	189	2	A6369	hypothetical prote
29	43.5	4.3	188	1	DDBPC2	dCMP deaminase (EC

30	43.5	4.3	188	2 S77089	hypothetical prote
31	43.5	4.3	188	2 D84468	hypothetical prote
32	43.5	4.3	189	2 S48914	hypothetical prote
33	43	4.2	189	2 E86707	transcription regu
34	43	4.2	189	2 JX0235	core protein MGC-2
35	42.5	4.2	188	2 S67051	hypothetical prote
36	42.5	4.2	188	2 AH2548	hypothetical prote
37	42.5	4.2	189	2 G90855	hypothetical prote
38	42.5	4.2	189	2 E69410	acetoin utilization
39	42	4.1	188	2 AB0878	probable membrane
40	42	4.1	188	2 S09789	hypothetical prote
41	42	4.1	188	2 S41600	adenomedullin - p
42	42	4.1	188	2 T46272	hypothetical prote
43	42	4.1	189	1 C1W01	insecticynin - to
44	42	4.1	189	2 AB0361	probable iron-sulp
45	41.5	4.1	188	2 B82183	ankk protein VC158

ALIGNMENTS

RESULT 1
159421
mast cell function associated antigen - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I59421
R/Gutmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A/Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A/Reference number: I59421, MUID:96016176, PMID:7568140
A/Accession: I59421
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-188 <RES>
A/Cross-references: UNIPROT:Q64335; UNIPARC:UPI000030101; EMBL:X79812; NID:G1020141; P
A/Gene: mafa

Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best local Similarity 53.5%; Pred. No. 5.5e-42;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY	1	MTDVSVIYSMLLPATQAQNDYGPQKSSSKSCGCVATITGLTAVLSTLVYQWIL	60
DB	1	MADNSIYSTLELPAPRVDDSRKAVAHRCVSYLVVVALGLTVILMSLLYQRTL	60
QY	61	COGSNVTGASCPSPDRMKYGNHCYFSEKEDMNSILEPCLARDSHLVTINDQEMS	120
DB	61	CCSGKGFMCQSCRCRPLMKRNSHCYTFEMEKRDNSSLKFCADKSHLTFPDQGVN	120
QY	121	ILQVPLSEAFQWIGLRNNSGWRWEDGSPILNFSRISSNFVQTGAINKGLQASSCEVPL	180
DB	121	LPQVEYGEDFYWIGLRIDDMRWEDGPAISLS-ILSNSVYQKGTTHRCGLHASSCEVAL	179
QY	181	HGVCKKY 187	
DB	180	QWICEKV 186	

RESULT 2
T33623
hypothetical protein F40G9.10 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T33623
R/Graves, T.; Suterer, C.; Ozersky, P.
Submitted to the EMBL Data Library, October 1999
A/Description: The sequence of C. elegans cosmid F40G9.
A/Reference number: Z21378
A/Accession: T33623
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA

A:Residues: 1-188 <GRA>
 A:Cross-references: UNIPROT:O9T275; UNIPARC:UPI000007BD20; EMBL:AF099919; PIDD:ACC68804.
 A:Experimental source: strain Bristol N2; clone F40G9
 C:Genetics:
 A:Gene: CESP:F40G9.10
 A:Map position: 3
 A:introns: 63/3; 99/1; 113/3; 153/3

Query Match 9.0%; Score 92.5; DB 2; Length 188;
 Best Local Similarity 31.4%; Pred. No. 0.23;
 Matches 27; Conservative 10; Mismatches 32; Indels 17; Gaps 4;

QY 79 WMKYNHCYFVSVEKDNSSLEFCLARDSHLLVI---TDNOMSLQVFLSEA----- 129
 DB 54 WESYINFCYKSTARRANFNDANNACRSESELSHSLTENQFL----VQLSAAGNRVNS 109

QY 130 ---FCWIGL-RNNSGMRWEDSGPLNF 151
 DB 110 KTNVYMTGLIFENRREWSMTDGSVVNY 135

RESULT 3
 F69262
 hypothetical protein AF0102 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: F69262

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Godek, A.; Zhou, L.; Overberg, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997

A:Authors: Uteback, T.; Cordon, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Moose, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: F69262
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-188 <KLE>
 A:Cross-references: UNIPROT:O30134; UNIPARC:UPI000005722A; GB:AE001099; GB:AE000782; NID

Query Match 5.7%; Score 58; DB 2; Length 188;
 Best Local Similarity 34.5%; Pred. No. 3.9e+02;
 Matches 20; Conservative 4; Mismatches 16; Indels 18; Gaps 2;

QY 118 EMSLLQVF-----LSEAFWIGLRNNSGMRWEDSGPLNRSISNSFVOTCAINKNG 170
 DB 14 KMRLLKLMKMDLSBISCEIGLRKQ-----SLPHKFLNTFGLIERNG 58

RESULT 4
 T27306
 hypothetical protein Y68A4B.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27306

R:Matthews, L.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z20341
 A:Accession: T27306
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-189 <WIL>
 A:Cross-references: UNIPROT:Q9X8X7; UNIPARC:UPI0000080A07; EMBL:AL023851; PIDD:CAA19555.
 A:Experimental source: clone Y68A4B
 A:Gene: CESP:Y68A4B.2
 A:Map position: 5
 A:introns: 21/1; 41/3; 78/1

Query Match 5.4%; Score 55.5; DB 2; Length 189;
 Best Local Similarity 19.8%; Pred. No. 6.7e+02;
 Matches 25; Conservative 14; Mismatches 42; Indels 45; Gaps 5;

QY 75 CPDRMK-----YGNHCY-----FVSEKDNSSLEFCLARDSHLLVITDNOEMSLQVF 125
 DB 23 CPTGAGQDERPSPGWCICKAFRDGCIOTYDAQA---CGAGAYLSGIQNVENQMMAGL 79

QY 126 LSEAFWIGLRNNS-----GMRWEDSGPLNFSRIS 155
 DB 80 AMTGCHWLGARRTAACIGQLVATCTRLNSFEWTDGATGDFWRLSDGEPNN---LF 136

QY 156 SNSFVQ 161
 DB 137 LNVFTQ 142

RESULT 5
 A39185
 virulence protein pagC precursor - Salmonella typhimurium
 C:Species: Salmonella typhimurium
 C:Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 09-Jul-2004
 C:Accession: A39185

R:Pulkkinen, W.S.; Miller, S.I.
 J. Bacteriol. 173, 86-93, 1991
 A:Title: A Salmonella typhimurium virulence protein is similar to a Yersinia enterocolit
 A:Reference number: A39185; MUID:91100323; PMID:1846140
 A:Accession: A39185

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-188 <PUL>
 A:Cross-references: UNIPROT:P23988; UNIPARC:UPI000014786E; GB:M55546; NID:q154232; PIDD:
 C:Superfamily: phage lambda membrane protein Iom

Query Match 5.4%; Score 55; DB 2; Length 188;
 Best Local Similarity 36.8%; Pred. No. 7.4e+02;
 Matches 14; Conservative 9; Mismatches 9; Indels 6; Gaps 2;

QY 138 NSGMRWEDSGPLNFSRISNSFV---QTCAINKNG 171
 DB 50 NVKRYEDSDSPVSF--ISLSYLVGDRQAGSGSVEPEGI 85

RESULT 6
 T19559
 hypothetical protein C29F3.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T19559

R:Matthews, L.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19142
 A:Accession: T19559
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-189 <WIL>
 A:Cross-references: UNIPROT:O17613; UNIPARC:UPI00000783D6; EMBL:Z81043; PIDD:CAB02800.1;
 A:Experimental source: clone C29F3
 A:Gene: CESP:C29F3.4
 A:Map position: 5
 A:introns: 32/3; 133/3

Query Match 5.4%; Score 55; DB 2; Length 189;
 Best Local Similarity 29.7%; Pred. No. 7.5e+02;
 Matches 11; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

QY 73 PSCPRMKY---GNHCYFVSVEKDNSSLEFCLA 105
 DB 33 PVPAGWFOFORATGTCYIFATPGAGWTTPOAACQA 69

RESULT 7
 ERAD75
 early E3 20.6K glycoprotein - human adenovirus 7 (strain Gomen)
 C:Species: Mastadenovirus h7 (human adenovirus 7)

C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 07-Nov-1997
 A.Name: host Homo sapiens (man)
 C.Accession: AJ1830
 R.Hong, J.S.; Mullis, K.G.; Engler, J.A.
 Virolology 167, 545-553, 1988
 A.Title: Characterization of the early region 3 and fiber genes of Ad7.
 A.Reference number: A94386; MUID:89073758; PMID:2849239
 C.Accession: AJ1830
 A.Molecule type: DNA
 A.Residues: 1-189 <HON>
 A.Cross-references: UNIPARC:UPI00001749B3; GB:M23696; NID:g341012
 A.Note: the Genbank entry ADR47FIBER PID:g576456 differs from the published sequence in
 C.Keywords: early protein; glycoprotein
 F.73.137/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.3%; Score 54.5; DB 1; Length 189;
 Best Local Similarity 23.5%; Pred. No. 8.3e+02;
 Matches 20; Conservative 19; Mismatches 13; Indels 33; Gaps 5;

QY 3 DSVYSMLEPPTQAOVDGPOO---KSSSSKSPS---GSCUVAI----- 41
 Db 89 DSDVDNIIVPAPATSA-----PRKTFSSSSAKASTIPKTSAMKLOKIALNSTAPK 143
 QY 42 -----TLGLTAVLAVSLVLYQWIIIC 61
 Db 144 TLPKSTIGITAVVGLIIT--FLC 166

RESULT 8
 D82719
 tryptophan repressor binding protein Xfl133 [imported] - Xylella fastidiosa (strain 9a5c
 C.Species: Xylella fastidiosa
 C.Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C.Accession: D82719
 R.anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A.Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A.Reference number: A82515; MUID:203657117; PMID:10910347
 A.Note: for a complete list of authors see reference number A59328 below
 A.Accession: D82719
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-189 <SIM>
 A.Cross-references: UNIPROT:Q9EP95; UNIPARC:UPI0000C2626; GB:AE003949; GB:AE003849; NID
 A.Experimental source: strain 9a5c
 R.Blimson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briston, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 de-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 Submitted to Genbank, June 2000
 A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kltajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 Chado, M.A.; Madeira, A.M.B.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
 A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.U. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
 M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A.Reference number: A59328
 A.Contents: annotation
 C.Genetics:
 A.Gene: Xfl133
 C.Superfamily: flavodoxin

Query Match 5.3%; Score 54.5; DB 2; Length 189;
 Best Local Similarity 26.1%; Pred. No. 8.3e+02;
 Matches 18; Conservative 8; Mismatches 29; Indels 9; Gaps 1;

QY 116 NOEMSLQVFLSEAFQWIGLRNNSGWRWEDGSPPLNFSRISSNSFYOTCGAINNGLOASS 175
 Db 106 NSLMSVTLFAAQHGHIWGLDLPNGNNSSTGSPNDLNRIGSWLGVMT-----QANN 156
 QY 176 CEVP 179

```

Db      157 DEAP 160

RESULT 9
JC5394
D/J-1 protein - human
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C:Accession: JC5394
R:Nagakubo, D.; Taira, T.; Kikura, H.; Ikeda, M.; Tamai, K.; Iguchi-Arigo, S.M.M.; Arii,
Biotech. Biophys. Res. Commun. 231, 509-513, 1997
A>Title: D/J-1, a novel oncogene which transforms mouse NIH3T3 cells in cooperation with
A:Reference number: JC5394; MUID:97223489; PMID:9070310
A:Accession: JC5394
A:Molecule type: mRNA
A:Residues: 1-189 <NMG>
A:Cross-references: UNIPROT:Q99497; UNIPARC:UPI0000072609; DBBJ:D61380; NID:G914937; PIR:
C:Comment: This protein is involved in a Ras-related signal transduction pathway.
C:Genetics:
A:Gene: GDB:DJ1
A:Cross-references: GDB:175839; OMIM:602533

Query Match      5.1%; Score 52; DB 1; Length 189;
Best Local Similarity 31.9%; Pred. No. 1.4e+03;
Matches 23; Conservative 9; Mismatches 26; Indels 14; Gaps 4;

QY      44 GLTAVLV--SVLLQWILCOGSNYSFSCASCPCSPDRMKYGNHCYFVSVEKDM----- 96
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      100 GLIAITCGPTALLAHEIGC-GSKYTT---HPLAKDKRMNGHITYSENRYEKDGLILTS 155
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      97 --NSLFECLA 105
      :||::||
Db      156 RGPSTSEFFALA 167

RESULT 10
BRAD35
early E3 20.5K glycoprotein - human adenovirus 3
C:Species: Mastadenovirus h3 (human adenovirus 3)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: F29500
R:Signaes, C.; Akusjaervi, G.; Petersson, U.
Gene 50, 173-184, 1986
A>Title: Region E3 of human adenoviruses; differences between the oncogenic adenovirus-
A:Reference number: A91566; MUID:87219876; PMID:3582978
A:Accession: F29500
A:Molecule type: DNA
A:Residues: 1-189 <SIG>
A:Cross-references: UNIPROT:P11322; UNIPARC:UPI0000129ADF; GB:M15952; NID:G209901; PIDN
A>Note: the authors translated the codon ATG for residue 161 as Ile and TTG for 165 as
C:Superfamily: adenovirus early E3 20.5K glycoprotein
C:Keywords: early protein; Glycoprotein
F.73.137/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      4.8%; Score 49.5; DB 1; Length 189;
Best Local Similarity 22.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 20; Mismatches 13; Indels 33; Gaps 5;

QY      3 DSVIISMELPPTATQANDYGPQ--KSSSKSPS-----CSCLVAI----- 41
      :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      89 NSLDVNIIVVPTATSA-----PRKSTFSSSSAKASTIPKTSAMDKLPKIALSNSTAAVN 143
      :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      42 -----TLGLTAVLVSLVLLQWILC 61
      :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      144 TIPKSTIGITAVVGLMI--FLC 166

RESULT 11
SS2803
hypothetical protein, 20.5K - human adenovirus 7
C:Species: Mastadenovirus h7 (human adenovirus 7)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

```

Accession: S52803
R:Kajon, A.E.; Wadell, G.
submitted to the EMBL Data Library, April 1995
A:Description: Sequence analysis of the E3 region and fiber gene of human adenovirus 7h.
A:Reference number: S52798
A:Accession: S52803
A:Molecule type: DNA
A:Residues: 1-189 <KAJ>
A:Cross-references: UNIPROT:Q83119, UNIPARC:UPI0000F8076, EMBL:Z48954, NID:G762955, PMID:11756682
C:Superfamily: adenovirus early E3 20.5K glycoprotein

Query Match 4.8%; Score 49.5; DB 2; Length 189;
Best Local Similarity 22.4%; Pred. No. 2.4e+03;
Matches 19; Conservative 20; Mismatches 13; Indels 33; Gaps 5;

Db 89 NSLDYNIIVPATYSA-----PRKSTPSSSAKASTIPKATSAITLKPKIALSNSTAPN 143
42 -----TIGLITPAVLISVLVQMIIC 61
||:||||:|:|
144 TIRKSTIGITPAVVGIMIT--FLC 166

RESULT 12
AE1446
probable scaffolding protein (Bacteriophage A116) lin0108 [imported] - Listeria innocua
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
A:Accession: AE1446
R:Glaser, P.; Fraigneul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Makarewicz, J.; Schneider, T.; Simoes, N.; Tlzer, A.; Vazquez-Boland, J.A.; Vose, H.; Wehland, A.
A>Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1446
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <GLA>
A:Cross-references: UNIPROT:Q92PJ6, UNIPARC:UPI0000CC10B; GB:AL592022; PIDN:CAC95341.1
A:Experimental source: strain Clij1262
C:Genetics:
A:Gene: lin0108

Query Match 4.8%; Score 49.5; DB 2; Length 189;
Best Local Similarity 23.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 13; Mismatches 24; Indels 21; Gaps 3;

Db 87 YFVSVEEKDNNSLEFLCAR-----DSHLVITD-----NQMSILOVPLS 127
||:||||:|:|
86 YQSEIAETKKNASALELASAKAKPKAVRALNDKLEITDEGLKGLDEQLAQE--s 143

Query 128 EAFWIGLRNNSGWRM 143
||:|:|:|:|:|
Db 144 DAYFAQESGNSALKW 159

RESULT 13
AH3634
more protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
A:Accession: AH3634
R:DelVecchio, V.G.; Kaparat, V.; Redkar, R.D.; Patra, G.; Mujer, C.; Los, T.; Ivanova, A.; Mazur, M.; Goldsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, A.
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3634

A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-189 <KUR>
A.Cross-references: UNIPROT:O8YB99; UNIPARC:UPI00000568d6; GB:AEO08918; PIDs:RAL54243.1;
A.Experimental source: strain 16M
C.Genetics:
A.Gene: BMEI11001
A.Map position: II

Query Match
Best Local Similarity 4.7%; Score 48.5; DB 2; Length 189,
Matches 16; Conservative 13; Mismatches 19; Indels 17; Gaps 4;

OY 92 BEKD-----WNSLEFCLARDSHLV-ITDNOEKSLQVFLSEAFWCIGLANN---- 138
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 19 BEEDSLLMLVLWMSELITFAILLDAFMWSVDPOGGLRAHLSPG---LAATNTVILL 75
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

OY 139 -SGWR 142
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 76 MSGWQ 80
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 14
AC1355
methylphosphotriester-DNA alkyltransferase and transcription regulator homolog lmo2243 [
C.Species: *Listeria monocytogenes*
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Accession: AC1355
R.Glaaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker,
J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.
D.; Jones, L.W.; Karst, U.
Science 294, 849-852, 2001
A.Authors: Kreffe, J.; Kuhn, M.; Kunet, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A.Title: Comparative genomics of *Listeria species*.
A.Reference number: AB1077; MUID:21537279; PMID:11679669
A.Accession: AC1355
A>Status: preliminary
A.Molecule type: DNA
A.Residues: 1-188 <GLA>
A.Cross-references: UNIPROT:O8Y533; UNIPARC:UPI000000C1EE; GB:NC_003210; PIDN:CAD00321.1
A.Experimental source: strain EGP-e
C.Genetics:
A.Gene: lmo2243
C.Superfamily: methylphosphotriester-DNA methyltransferase; methylphosphotriester-DNA me

Query Match
Best Local Similarity 4.7%; Score 48; DB 2; Length 188;
Matches 17; Conservative 12; Mismatches 34; Indels 2; Gaps 2;

OY 67 STCASCC-PSCPDPRMWKYGNGHCYFSVEBKDNSSLFECLARDSHLVITDNOEKSLLQVF 125
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 31 STRIKCYPECKSRLPKENIVIFHSAEA-FSHGYARACKRKCSGSALPDIEMVNNIEMY 89
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

OY 126 ISEAF 130
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 90 IKENF 94
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 15
H90106
60S ribosomal protein L9 [imported] - Guillardia theta nucleomorph
C.Species: nucleomorph Guillardia theta
A.Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C.Accession: H90106
R.Douglas, S.; Zauner, S.; Fraunholz, W.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A>Title: The highly reduced genome of an enslaved algal nucleus.
A.Reference number: A99082; MUID:11323671; PMID:11323671
A.Accession: H90106
A.Status: preliminary
A.Molecule type: DNA

U.S. Bank (USPO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 14:41:26 ; Search time 87.5115 Seconds
(without alignments)
943.913 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036

Sequence: 1 MADNSIYSTLELPAAPRVQD.....GLHSSCEVALQICEKILP 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 6014

Minimum DB seq length: 188

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	AAR77033 Mammalian
2	1036	100.0	188	2	AAW88277 Rat mast
3	1036	100.0	188	4	AAE11761 Rat mast
4	838	80.9	188	4	AAE11760 Mouse mas
5	545.5	52.7	189	7	ADDD25635 Binding d
6	545.5	52.7	189	9	ADY19892 PRO polyp
7	525.5	50.7	189	2	AAW88265 Human mas
8	525.5	50.7	189	4	AAE11759 Human mas
9	164.5	15.9	188	9	AAE89021 Chicken M
10	159.5	15.4	188	4	AAW78675 Human pro
11	159.5	15.4	188	4	AAU00671 Human INT
12	159.5	15.4	188	6	ABO32533 Secreted
13	159.5	15.4	188	7	ADP65310 Human C-t
14	159.5	15.4	188	8	ADQ10144 Human pol
15	159.5	15.4	188	8	ADP25141 PRO polyp
16	153.5	14.8	189	4	AAU19837 Human nov
17	153.5	14.8	189	5	ABBI17910 Human ner
18	153.5	14.8	189	5	ABP48057 Human pol
19	153.5	14.8	189	7	ADCI1019 Human pro
20	92.5	8.9	188	4	ABBS9566 Drosophila
21	80.5	7.8	189	9	ABE70262 E-selectin
22	75.5	7.3	188	4	ABBS8823 Drosophila
23	75.5	7.3	189	7	ADC38690 Human sec
24	60	5.8	188	3	AAE60348 Arabidops

25	60	5.8	188	3	AAI19860 Arabidops
26	60	5.8	188	4	AAW39399 Human pol
27	59.5	5.7	188	8	ADN22989 Bacterial
28	56	5.4	188	3	AAE23544 Cytokine
29	56	5.4	189	5	ABBA7756 Listeria
30	55.5	5.4	189	6	ABBU01363 S. pneumo
31	55	5.3	189	6	ABU11464 Human MDP
32	55	5.3	189	8	ADK68097 Plant ful
33	54	5.2	189	3	AAI19506 Arabidops
34	53.5	5.2	188	5	ABE70315 Human MDP
35	53.5	5.2	188	2	AAI35751 Chlamydia
36	53.5	5.2	189	4	AAE65153 Basic fib
37	52.5	5.1	188	8	ADK74859 Plant ful
38	52	5.0	188	5	ABBA48274 Listeria
39	52	5.0	188	8	ADT48905 Oll-asso
40	50.5	4.9	188	3	AAE6736 Arabidops
41	50.5	4.9	188	4	AAU23356 Novel hum
42	50	4.8	188	3	AAU07314 Arabidops
43	50	4.8	188	8	ADK88330 Plant ful
44	48.5	4.7	189	1	AAI30179 Sequence
45	48.5	4.7	189	1	AAI40123 Sequence

ALIGNMENTS

RESULT 1
AAR77033
ID / AAR77033 standard; protein; 188 AA.

XX AAR77033;
AC AAR77033;
DT 01-FEB-1996 (first entry)
XX
DE Mammalian mast cell function-associated antigen (MAFA).
XX
KW Mast cell function-associated antigen; MAFA; soluble; ligand;
KW identification; screening; inflammation; inflammatory; allergic;
KW prevention.
XX
XX Rattus rattus.
OS
XX
PN WO9527734-A1.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US004258.
XX
PR 08-APR-1994; 94IL-00109257.
XX
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX (RYCU/) RYCU A.
XX
PI Pecht I, Gutmann MD, Tal M;
XX
DR WPI; 1995-366356/47.
XX
DR N-PSDB; AAT01471.
XX

PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -
PT useful for screening for ligands of MAFA which are useful for prevention
PT of inflammatory and allergic reactions.
XX
PS Claim 12; Page 37; 54pp; English.

XX A soluble form of mast cell function-associated antigen (MAFA) can be
XX produced by recombinant techniques for use in the ligand- screening
XX assay. The ligands that are identified may be used alone or in
XX combination with the MAFA to prevent inflammatory and allergic reactions
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 3e-96;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADNSYSTLELPAAPRVQDDSRMKVKAHLRPCVSYLVMAALGLTITLMSLLYQRTL 60
   |||||
Db 1 MADNSYSTLELPAAPRVQDDSRMKVKAHLRPCVSYLVMAALGLTITLMSLLYQRTL 60
QY 61 CCGSGFMCSCQSRCPNLMNRNGSHCYFSEMEKRDWNSLKFCDKXSHLLTFPNQGVN 120
   |||||
Db 61 CCGSGFMCSCQSRCPNLMNRNGSHCYFSEMEKRDWNSLKFCDKXSHLLTFPNQGVN 120
QY 121 LFOEYVGEDFYWIGLRDIDGRMEDGPAISLSISNSVYQKCGTTHRCGLHASSCEVALQ 180
   |||||
Db 121 LFOEYVGEDFYWIGLRDIDGRMEDGPAISLSISNSVYQKCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVLTP 188
   |||||
Db 181 WICEKVLTP 188
```

RESULT 2

AAW88277
ID AAW88277 standard; protein; 188 AA.

XX AAW88277;

DT 29-MAR-1999 (first entry)

DE Rat mast cell function-associated antigen (MAFA).

KW Mast cell function-associated antigen; MAFA; splice variant; rat;
inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

OS Rattus sp.

PH Key Location/Qualifiers

FT Modified-site 82..84 /note= "Asn is N-glycosylated"

FT Modified-site 97..99 /note= "Asn is N-glycosylated"

XX W09854209-A2.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-GB001572.

XX 31-MAY-1997; 97GB-00011148.

XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Hewitt EL, Lamere MBAC, Lamont A, Williams DH;

XX WPI; 1999-059806/05.

XX N-PSDB; AAW84222.

PT New polypeptide having a sequence corresponding to human mast cell
function-associated antigen - useful in forming and manufacturing
pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.

PS Disclosure; Fig 4; 44pp; English.

CC This is the amino acid sequence of rat mast cell function-associated
antigen (MAFA), a type II membrane glycoprotein found on mast cells and
basophils. The invention relates to cloning of the human MAFA molecule
(see AAW88265) and to the discovery of splice variants (see AAW88266-67)
of human MAFA that are not found in rat. Polypeptides and synthetic
peptides (see AAW88258-64) based on human MAFA and human truncated MAFA,
CC and polynucleotides encoding them, can be used in methods for the
treatment of inflammatory and allergic diseases (e.g. rheumatoid
arthritis and asthma), and tumour growth

XX Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 3e-96;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADNSYSTLELPAAPRVQDDSRMKVKAHLRPCVSYLVMAALGLTITLMSLLYQRTL 60
   |||||
Db 1 MADNSYSTLELPAAPRVQDDSRMKVKAHLRPCVSYLVMAALGLTITLMSLLYQRTL 60
QY 61 CCGSGFMCSCQSRCPNLMNRNGSHCYFSEMEKRDWNSLKFCDKXSHLLTFPNQGVN 120
   |||||
Db 61 CCGSGFMCSCQSRCPNLMNRNGSHCYFSEMEKRDWNSLKFCDKXSHLLTFPNQGVN 120
QY 121 LFOEYVGEDFYWIGLRDIDGRMEDGPAISLSISNSVYQKCGTTHRCGLHASSCEVALQ 180
   |||||
Db 121 LFOEYVGEDFYWIGLRDIDGRMEDGPAISLSISNSVYQKCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVLTP 188
   |||||
Db 181 WICEKVLTP 188
```

RESULT 3

AAE11761
ID AAE11761 standard; protein; 188 AA.

XX AAE11761;

DT 18-DEC-2001 (first entry)

DE Rat mast cell function associated antigen (MAFA) protein.

KW Rat; pharmaceutical composition; mast cell function associated antigen;
MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
immunosuppressive; cytostatic.

OS Rattus norvegicus.

XX W0200170805-A2.

XX 27-SEP-2001.

XX 16-MAR-2001; 2001WO-US0008596.

XX 17-MAR-2000; 2000US-0190716P.

XX (GEMI-) GEMINI SCI INC.

XX Takahashi N, Mikayama T;

XX WPI; 2001-611482/70.

XX N-PSDB; AAD18736.

PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
to mast cell function-associated antigen ligand on target cell.

PS Example 1; Page 19; 49pp; English.

CC The present invention relates to a pharmaceutical composition comprising
an agent which specifically binds to a mast cell function associated
antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
ligand and a pharmaceutically acceptable excipient. The invention is
useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
binding to a ligand on a target cell, by contacting the pharmaceutical
composition in vitro, ex vivo or in vivo by administering the composition
to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
an amount sufficient to inhibit cell surface MAFA binding to the ligand
on the target cell. The agent or the composition is useful for treating a
tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of

CC NK cell or a T-cell. The present sequence is rat MAFa protein
XX
SQ Sequence 188 AA;

Query Match 100.0%; Score 1036; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 3e-96;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSYSTLELPAAPRVDDSRMKVAVLHRCVSYLVMAVGLITVIMSLLYORTL 60
DB 1 MADNSYSTLELPAAPRVDDSRMKVAVLHRCVSYLVMAVGLITVIMSLLYORTL 60
QY 61 CCGSKGFMCSQCSRCPNLMWRNGSHCYFSMEKRDWNSLTKFCADKGSHTLPDPNOGVN 120
DB 61 CCGSKGFMCSQCSRCPNLMWRNGSHCYFSMEKRDWNSLTKFCADKGSHTLPDPNOGVN 120
QY 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPAISLISNSVVOCKGTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPAISLISNSVVOCKGTHRCGLHASSCEVALQ 180
QY 181 WICEKVL 188
DB 181 WICEKVL 188

RESULT 4

AAE11760
ID AAE11760 standard; protein; 188 AA.

AAE11760;

18-DEC-2001 (first entry)

Mouse mast cell function associated antigen (MAFA) protein.

XX Mouse; pharmaceutical composition; mast cell function associated antigen;
KW MAFa; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KM immunosuppressive; cyclostatic.

XX Mus sp.

XX Key Location/Qualifiers
FH Domain 64..188
FT /note= "Extracellular domain"

PN W0200170805-A2.

PD 27-SEP-2001.

PF 16-MAR-2001; 2001WO-US008596.

PR 17-MAR-2000; 2000US-0190716P.

XX (GEMT-) GEMINI SCI INC.

XX Takahashi N, Mkyama T;

XX WPI; 2001-611482/70.

XX N-PSDB; AAD18735.

PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
PT to mast cell function-associated antigen ligand on target cell.

XX Example 1; Page 19; 49pp; English.

XX The present invention relates to a pharmaceutical composition comprising
CC an agent which specifically binds to a mast cell function associated
CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
CC killer (NK) or T-cell-expressed cell surface MAFa from binding to MAFa
CC ligand and a pharmaceutically acceptable excipient. The invention is
CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFa
CC binding to a ligand on a target cell, by contacting the pharmaceutical

CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFa binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is mouse MAFa protein
XX
SQ Sequence 188 AA;

Query Match 80.9%; Score 838; DB 4; Length 188;
Best Local Similarity 80.7%; Pred. No. 3.1e-76;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSYSTLELPAAPRVDDSRMKVAVLHRCVSYLVMAVGLITVIMSLLYORTL 60
DB 1 MADNSYSTLELPAAPRVDDSRMKVAVLHRCVSYLVMAVGLITVIMSLLYORTL 60
QY 61 CCGSKGFMCSQCSRCPNLMWRNGSHCYFSMEKRDWNSLTKFCADKGSHTLPDPNOGVN 120
DB 61 CCGSKGFMCSQCSRCPNLMWRNGSHCYFSMEKRDWNSLTKFCADKGSHTLPDPNOGVN 120
QY 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPAISLISNSVVOCKGTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGEDFYWIGLRDIDGMRWEDGPAISLISNSVVOCKGTHRCGLHASSCEVALQ 180
QY 181 WICEKVL 187
DB 181 WICEKVL 187

RESULT 5
ADD25635
ID ADD25635 standard; protein; 189 AA.

ADD25635;

15-JUN-2004 (first entry)

Binding domain-immunoglobulin fusion protein-associated protein #95.

XX Binding domain; immunoglobulin; fusion protein; cyclostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

PN US2003118592-A1.

XX 26-JUN-2003.

XX 25-JUL-2002; 2002US-00207655.

XX 17-JAN-2001; 2001US-0367358P.

XX 17-JUN-2002; 2002US-00053530.

XX 03-JUN-2002; 2002US-0385691P.

XX (GENE-) GENERAFT INC.

XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX WPI; 2003-801317/75.

XX New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.

PS Disclosure; SEQ ID NO 196; 157pp; English.

CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.

XX SQ Sequence 189 AA;

Query Match 52.7%; Score 545.5; DB 7; Length 189;

Best Local Similarity 55.1%; Pred. No. 1.1e-46;

Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIVSTLELPAAAPRVODDSRMKVKAVLHRCVSYLVMAALGLTIVIMSLTYQRTL 60
DB 1 MTDVSIYSLMLPRTAQNDYGPQKSSSRPSCVLAIALGLTIVLVSLLYQWTL 60
QY 61 CCGSKGFMCSCQSRCPNIMRNNGSHCYFSEMEKRDWNSLKFCAADKSHLLTFPDNGVN 120
DB 61 CCGSNVSTCASCPCSPCDRMKYGNNHCYFSEMEKDNSSLFECCLARDSHLLVITDNOEWS 120
QY 121 LFGVYGEDPFYWGIGRIDGKRWEDGPAISLS-ILSNVYQKCGTIHRCGLAASCEVAL 179
DB 121 LLOVFLSEAFWIGIRNNSGMRWEDGSPINFSRISNSFVQTCGAINKGLQASSCEVPL 180
QY 180 QWICEKV 186
DB 181 HMVCKKV 187

RESULT 6
ADY19892
ID ADY19892 standard; protein; 189 AA.

XX ADY19892;
DT 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 5698.

DE Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Anticancer; Osteoporosis; Hemostatic; Anticancer;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Anticancer; Gastrointestinal-Gen.; Antipsychotic; Anticancer;
XX Anticancer; diagnosis.

XX Homo sapiens.

XX WO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GETH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 8; SEQ ID NO 5698; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX composition, and method are useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis. The present sequence represents a PRO polypeptide.

XX SQ Sequence 189 AA;

Query Match 52.7%; Score 545.5; DB 9; Length 189;

Best Local Similarity 55.1%; Pred. No. 1.1e-46;

Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIVSTLELPAAAPRVODDSRMKVKAVLHRCVSYLVMAALGLTIVIMSLTYQRTL 60
DB 1 MTDVSIYSLMLPRTAQNDYGPQKSSSRPSCVLAIALGLTIVLVSLLYQWTL 60
QY 61 CCGSKGFMCSCQSRCPNIMRNNGSHCYFSEMEKRDWNSLKFCAADKSHLLTFPDNGVN 120
DB 61 CCGSNVSTCASCPCSPCDRMKYGNNHCYFSEMEKDNSSLFECCLARDSHLLVITDNOEWS 120
QY 121 LFGVYGEDPFYWGIGRIDGKRWEDGPAISLS-ILSNVYQKCGTIHRCGLAASCEVAL 179
DB 121 LLOVFLSEAFWIGIRNNSGMRWEDGSPINFSRISNSFVQTCGAINKGLQASSCEVPL 180
QY 180 QWICEKV 186
DB 181 HMVCKKV 187

RESULT 7
AAW88265
ID AAW88265 standard; protein; 189 AA.

XX AAW88265;

XX 29-MAR-1999 (first entry)

XX Human mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA, splice variant; human,
XX inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 7..10
FT /note="ITIM motif"
FT Modified-site 65..67
FT /note="Asn is N-glycosylated"
FT Modified-site 97..99
FT /note="Asn is N-glycosylated"
FT Modified-site 137..139
FT /note="Asn is N-glycosylated"
FT Modified-site 150..152
FT /note="Asn is N-glycosylated"
XX
XX WO9654209-A2.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-GB001572.
XX
XX 31-MAY-1997; 97GB-00011148.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Hewlett EL, Lamers MBAC, Lamont A, Williams DH;
XX
XX WPI; 1999-059806/05.
XX N-PSDB; AAV84198.
XX
XX New polypeptide having a sequence corresponding to human mast cell
PT function-associated antigen - useful in forming and manufacturing
PT pharmaceutical compositions in the treatment of inflammatory and allergic
PT diseases, and tumour growth.
XX
XX Disclosure; Fig 1; 44pp; English.
XX
XX This is the amino acid sequence of human mast cell function- associated
CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198)
CC encoding human MAFA can be obtained from myelogenous leukaemic cell line
CC KU812 or cDNA derived from human lung tissue. The encoded protein is
CC similar to the rat form (see AAV88277) having an intracellular domain
CC containing a putative immunoreceptor tyrosine activation motif (ITIM) and
CC an extracellular lectin-like domain. 2 Alternatively spliced forms (see
CC AAV88266-67) of human MAFA have been identified. Polypeptides and
CC synthetic peptides (see AAV88258-64) based on these truncated MAFA
CC proteins can be used in methods for the treatment of inflammatory and
CC allergic diseases, and tumour growth
XX
XX Sequence 189 AA;
SQ

Query Match 50.7%; Score 525.5; DB 2; Length 189;
Best Local Similarity 53.5%; Pred. No. 1.2e-44;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MADNSIYSTELEPAAPRVODDSRMKVAVALHRPCSVLYVWALGLTVIIMSLLYQRTL 60
DB 1 MTSVSIYSMELPATAQNDYGPQKSSSKSCCLVAITGLTAVALLSVLYQWIL 60
QY 61 CCSGKGMFCGQRCPCPLWMRNGSHCYFYSMEKRDNNSSLKFCADKSHLLTPPDNGVN 120
DB 61 CCGSNYSTCASCPCPRMWMKYGNHCYFYSVEEKDNNSSLEFCLARDSHLLVTTDNGMS 120
QY 121 LPOEYVEDPFWYIGLRDIDGMRWEDGPALSLTSLNSVYQKCGTIRHCGIHAASCEVAL 179
DB 121 LLOVFLSEAFQWIGLRNNSGMRWEDGSPILNFSIRISSFVOTGAIKNGIQAASSCEVPL 180
QY 180 QWICEKV 186
DB 181 HGVCCKV 187

RESULT 8
AAE11759

ID AAE11759 standard; protein; 189 AA.
XX
XX AAE11759;
AC 18-DEC-2001 (first entry)
XX
XX
XX Human mast cell function associated antigen (MAFA) protein.
DE
XX Human; pharmaceutical composition; mast cell function associated antigen;
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW immunosuppressive; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCI INC.
XX
XX Takahashi N, Mikayama T;
PI
XX WPI; 2001-611482/70.
XX N-PSDB; AAD18734.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
PT to mast cell function-associated antigen ligand on target cell.
XX
XX Claim 10; Page 18; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
CC an agent which specifically binds to a mast cell function associated
CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
CC killer (NK) or T-cell-expressed cell surface MAFA from binding to MAFA
CC ligand and a pharmaceutically acceptable excipient. The invention is
CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
CC binding to a ligand on a target cell, by contacting the pharmaceutical
CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is human MAFA protein
XX
XX Sequence 189 AA;
SQ

Query Match 50.7%; Score 525.5; DB 4; Length 189;
Best Local Similarity 53.5%; Pred. No. 1.2e-44;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MADNSIYSTELEPAAPRVODDSRMKVAVALHRPCSVLYVWALGLTVIIMSLLYQRTL 60
DB 1 MTSVSIYSMELPATAQNDYGPQKSSSKSCCLVAITGLTAVALLSVLYQWIL 60
QY 61 CCSGKGMFCGQRCPCPLWMRNGSHCYFYSMEKRDNNSSLKFCADKSHLLTPPDNGVN 120
DB 61 CCGSNYSTCASCPCPRMWMKYGNHCYFYSVEEKDNNSSLEFCLARDSHLLVTTDNGMS 120
QY 121 LPOEYVEDPFWYIGLRDIDGMRWEDGPALSLTSLNSVYQKCGTIRHCGIHAASCEVAL 179
DB 121 LLOVFLSEAFQWIGLRNNSGMRWEDGSPILNFSIRISSFVOTGAIKNGIQAASSCEVPL 180
QY 180 QWICEKV 186
DB 181 HGVCCKV 187

RESULT 8
AAE11759

QY 182 ICEK 185
 DB 182 ICEK 185

RESULT 11
 AA00671
 ID AA00671 standard; protein, 188 AA.
 AC AA00671;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human INTERCEPT 289 form 1a polypeptide.
 XX
 KM Human; INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain;
 KM skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;
 KM bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;
 KM anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease;
 KM malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
 KM attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
 KM hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
 KM muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 7..27
 FT /note="Transmembrane domain"
 FT Domain 28..188
 FT /note="Extracellular domain"

MO200123088-A1.
 26-APR-2001.
 23-JUN-2000; 2000MO-US017386.
 19-OCT-1999; 99US-00420707.
 (MILL-) MILLENNIUM PHARM INC.
 Mackay CR, Myers PS, Kirst SJ, Fraser CC, Leiby KR;
 WPI; 2001-308477/32.
 N-PSDB; AAS00661.

New isolated nucleic acid molecule for diagnosis, prevention, and therapy of human and other animal disorder, or as modulating agent for regulating cellular processes.

Claim 8; Fig 2A-2B; 263pp; English.

The sequence represents human INTERCEPT 289 form 1a polypeptide. This protein and similar others exhibit the ability to affect growth, proliferation, survival, differentiation, activity, morphology, or movement/migration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral blood leukocyte, bone marrow or thymus tissue. They can be used as modulating agents for regulating cellular processes, thus, the proteins and their associated nucleic acids can be used to prognosticate, prevent, diagnose, or treat disorders associated with physiological processes. These disorders include abnormal blood coagulation, asthma, anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis, meningitis, attention deficit disorder, Crohn's disease, gastroenteritis, goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and muscular dystrophy. Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immuno-competent vertebrate and harvesting blood or serum from the vertebrate

Sequence 188 AA;
 SQ

Query Match 15.4%; Score 159.5; DB 4; Length 188;
 Best Local Similarity 25.5%; Pred. No. 1.1e-07;
 Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;

QY 40 MVALGLTVIL-----MSLL-----YQRTLCGS-----KGFMS 70
 DB 5 MIISGLIVVVLKVGWTLFLFYFPOIFNKSNDGFTTTSYGTVSQIFGSSSPSPNGFIPT 64
 QY 71 QC--SRCPNLMRNNGSHCYFPMERDNSSILKPCADGSHLITPPDNGVNLFOEYGE 128
 DB 65 RSYGVCPDMEFYQARCFPLSTSSSMNESDPCCKGSTLAIVNTPKTLFLQDITDA 124
 QY 129 DFWYIGL---RDIDGWRWEDGPAISLISNSVVOCKGTIHRGCL---HASSCEVALQW 181
 DB 125 EKFTGLIHRBEKRRRWLNNSVFNQNTVNONFNRCATI---GLTKTFDASCDISYR 181

QY 182 ICEK 185
 DB 182 ICEK 185

RESULT 12
 ABO32533
 ID ABO32533 standard; protein, 188 AA.
 AC ABO32533;
 DT 17-SEP-2003 (first entry)
 XX
 DE Secreted polypeptide-related protein #18.

Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;
 KM hormonal disorder; proliferative disorder; cancer; thyroid disorder;
 KM diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
 KM Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KM myocardial infarction; congestive heart disease; blood platelet disorder;
 KM thrombocytopenia; blood vessel; atherosclerosis; vasculitis.

XX
 OS Homo sapiens.
 XX
 OS US2003022279-A1.
 XX
 PN 30-JAN-2003.
 XX
 PD 12-JAN-2001; 2001US-00759130.
 XX
 PE 14-JUN-1999; 99US-00333159.
 XX
 PR 29-JUN-1999; 99US-00342364.
 PR 10-SEP-1999; 99US-00393996.
 PR 19-OCT-1999; 99US-00420707.
 PR 07-JAN-2000; 2000US-00479249.
 PR 27-APR-2000; 2000US-00559497.
 PR 24-MAY-2000; 2000US-00578063.
 PR 16-JUN-2000; 2000US-00596194.
 PR 23-JUN-2000; 2000US-00602871.
 PR 30-JUN-2000; 2000US-00608452.
 XX
 XX (FRAS/) FRASER C C.
 PA (BARN) BARNES T M.
 PA (SHAR) SHARP J D.
 PA (KIRS) KIRST S J.
 PA (MYER) MYERS P S.
 PA (LEIB) LEIBY K R.
 PA (HOLT) HOLTZMAN D A.
 PA (MCCA) MCCARTHY S A.
 PA (WRI) WRIGHTON N.
 PA (MACK) MACKAY C R.
 PA (GOOD) GOODEARL A D J.
 XX
 XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
 XX WPI; 2003-456290/43.

DR N-PSDB; ACD66719, ACD66720.
XX
XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
PT treating disorders such as cancer, diabetes or atherosclerosis, and in
PT forensic biology.
XX
XX
PS Claim 9; Fig 11A-11C; 482pp; English.
XX
XX The invention relates to secreted polypeptide-related proteins and
CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
CC nucleic acids, proteins and antibodies specific to the proteins are
CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
CC prophylactic and therapeutic methods. The sequences are used in
CC diagnosing, preventing or treating proliferative disorders (e.g.
CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related protein of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC segdata.uspto.gov/sequence.html
XX
SQ Sequence 188 AA;
XX
Query Match 15.4%; Score 159.5; DB 6; Length 188;
Best Local Similarity 25.5%; Pred. No. 1.1e-07;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;
QY 40 MVALGLTLVIL---MSLL-----YQRTLCGS-----KGPMCS 70
DB 5 MISGLIVVLKVGWTLFLYFPQIFNKNDGFTTTSYGVQSI FGSSSPSPNGFITT 64
QY 71 QC--SRCPLUMRNOSHCHYFMSMKRDNSSLKPCADKSHLLTPPDNGVNLPEYVGE 128
DB 65 RSYGVCPKDMWEPFYQARCFPLSTSSWNESRDFCKGSTLAIVNTPDKLFLDITDA 124
QY 129 DEYWIGL---RDIDGRMEDGPAISLISNSVVKCGTIHRGCL---HASSCEVALQW 181
DB 125 EKYFGLIYHBEKRWKRINNSVFNQNTNQNPNCAIT---GLTKTPDASCDISYR 181
QY 182 ICEK 185
DB 182 ICEK 185
RESULT 13
ADP65310
ID ADP65310 standard; protein, 188 AA.
XX
XX ADP65310;
AC
XX 12-AUG-2004 (first entry)
DT
XX
XX Human c-type (calcium dependent, carbohydrate-recognition domain) lectin.
DE
XX
XX autoimmune disease; arthritis; gene expression analysis;
KM rheumatoid arthritis; collagen-induced; immunosuppressive; antineumatic;
KM antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KM immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
KM fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KM immune; human.
XX
XX Homo sapiens.
OS
XX WO2003072827-A1.
PN
XX 04-SEP-2003.
PD

XX
XX 31-OCT-2002; 2002WO-US035433.
PF
XX
XX 31-OCT-2001; 2001US-0336220P.
PK
XX
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
PA
XX
XX Hirsch R, Thornton SL;
PI
XX
XX WPI, 2003-712740/67.
DR
XX
XX GENBANK; NP_037384.
DR
XX
XX
PT Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX
XX Disclosure; Page; 56pp; English.
XX
XX The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritis. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritis in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification
CC of genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analysis of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antineumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritis, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This sequence represents a
CC protein sequence relating to the genes used in the analysis and treatment
CC of autoimmune diseases or arthritis. Note: This sequence is not shown
CC in the specification. It has been supplied in an electronic format from
CC WIPO.
XX
SQ Sequence 188 AA;
XX
Query Match 15.4%; Score 159.5; DB 7; Length 188;
Best Local Similarity 25.5%; Pred. No. 1.1e-07;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;
QY 40 MVALGLTLVIL---MSLL-----YQRTLCGS-----KGPMCS 70
DB 5 MISGLIVVLKVGWTLFLYFPQIFNKNDGFTTTSYGVQSI FGSSSPSPNGFITT 64
QY 71 QC--SRCPLUMRNOSHCHYFMSMKRDNSSLKPCADKSHLLTPPDNGVNLPEYVGE 128
DB 65 RSYGVCPKDMWEPFYQARCFPLSTSSWNESRDFCKGSTLAIVNTPDKLFLDITDA 124
QY 129 DEYWIGL---RDIDGRMEDGPAISLISNSVVKCGTIHRGCL---HASSCEVALQW 181
DB 125 EKYFGLIYHBEKRWKRINNSVFNQNTNQNPNCAIT---GLTKTPDASCDISYR 181
QY 182 ICEK 185
DB 182 ICEK 185
RESULT 14
ADQ10144
ID ADQ10144 standard; protein, 188 AA.
XX

XX ADQ10144;
XX 09-SEP-2004 (first entry)
XX Human polypeptide #25.
XX Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;
KW anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;
KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;
KW arteriosclerosis; hypertension; bacterial infection; psoriasis;
KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;
KW Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;
KW golter; infertility; endometriosis; muscular disorder.
XX Homo sapiens.
XX US2004121396-A1.
XX 24-JUN-2004.
XX 19-DEC-2003; 2003US-00741790.
XX 14-JUN-1999; 99US-00333159.
PR 29-JUN-1999; 99US-00342364.
PR 10-SEP-1999; 99US-00393996.
PR 19-OCT-1999; 99US-00420707.
PR 07-JAN-2000; 2000US-00479249.
PR 27-APR-2000; 2000US-00559497.
PR 24-MAY-2000; 2000US-00578063.
PR 16-JUN-2000; 2000US-00596194.
PR 23-JUN-2000; 2000US-00602871.
PR 30-JUN-2000; 2000US-00608452.
PR 12-JAN-2001; 2001US-00759130.
XX (MILL-) MILLENNIUM PHARM INC.
PA Frazer CC, Barnea TM, Sharp JD, Kirst SJ, Myers PG, Leiby KR;
PT Holzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodheart ADJ;
XX WPI; 2004-479675/45.
XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
PT treating cancer, constipation, hemorrhoids, cystic fibrosis,
PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
PT tuberculosis, malaria, golter, infertility.
XX Claim 9; SEQ ID NO 83; 483pp; English.
XX The invention relates to human polynucleotides and the polypeptides they
XX encode. The invention also relates to a host cell containing a
CC polynucleotide of the invention, an antibody which selectively binds with
CC a polypeptide of the invention, a method of detecting the presence of a
CC polypeptide in a sample, a method of identifying a compound which binds
CC with a polypeptide, and a method of modulating the activity of a
CC polypeptide. The polynucleotides, polypeptides and compositions are
CC useful for diagnosing, preventing and/or treating cancer, obesity, A
CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host
CC reactions, allergic reactions, cystic fibrosis, hypogonadism,
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
CC disease, AIDS, tuberculosis, viral infections, malaria, golter,
CC infertility, endometriosis, wounds and muscular disorders. This sequence
CC represents a human polypeptide of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX Sequence 188 AA;
SQ

Query Match 15.4%; Score 159.5; DB 8; Length 188;
Best Local Similarity 25.5%; Pred. No. 1.1e-07;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;

Oy		40	MVALGLTLVL-----MLLL-----YQRLTCCS-----KGFMCS	70
Dd		5	MISGLIVLVALKVGMFLFLFYPIQRNKSNDGFTTRSYGVQVIRCGSSSPNGFITT	64
Oy		71	QC--SRCPNLMMRNGSHCYFYSMEKRDWNSLKECADKGSHTLTFPDNGVNLFQEVYGE	128
Dd		65	RSYVTVEPKMPEFYQARCFPLSTSESSMNBSRDPCKSGSLTAIVMTPEKLKPLDITDA	124
Oy		129	DFWIGL---RDIDGMEDGPALSLSLNSVVQKCGTIHRCGL-----HASSCEVALQW	181
Dd		125	EKYFIGIHYHEEKRMRWMNNSVGNVMONFNCAFI---GLTYTFDPAASCDISTYR	181
Oy		182	ICEK 185	
Dd		182	ICEK 185	
 RESULT 15 ADP25141 ID ADP25141 standard; protein: 188 AA.				
XX				
AC			ADP25141;	
XX				
DT			18-NOV-2004 (first entry)	
XX				
DE			PRO polypeptide SEQ ID NO:2319.	
XX				
KW			PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;	
KW			osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;	
KW			antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.	
OS			Unidentified.	
PN			WO2004041170-A2.	
PD			21-MAY-2004.	
PF			30-OCT-2003; 2003WO-US034312.	
PR			01-NOV-2002; 2002US-0423394P.	
PA			(GETH) GENENTECH INC.	
PI			Clark H, Schenfeld J, Van Lookeren M, Williams PM, Wood WI;	
PI			Wu TD;	
DR			WPI; 2004-419628/39.	
XX			N-PESDB; ADP25140.	
PT			New PRO polypeptides and polynucleotides, useful for treating e.g.	
PT			erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated	
PT			renal disease, or demyelinating diseases of the central or peripheral	
PT			nervous system.	
PS			Claim 7; SEQ ID NO 2319; 2940pp; English.	
XX				
CC			The invention relates to a novel isolated nucleic acid and the PRO	
CC			polypeptide encoded by it. A protein of the invention has	
CC			antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,	
CC			osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,	
CC			antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide	
CC			of the invention may have a use in gene therapy. The PRO polypeptide, its	
CC			agonist, antagonist or antibody that specifically binds to the	
CC			polypeptide is useful for treating an immune related disorder such as	
CC			systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, an	
CC			juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an	
CC			idiopathic inflammatory myopathy, Sjogren's syndrome, systemic	
CC			vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune	
CC			chromocytoma, thyroiditis, diabetes mellitus, immune-mediated renal	
CC			disease, a demyelinating disease of the central or peripheral nervous	
CC			system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,	
CC			a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary	

CC disease infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.

SQ Sequence 188 AA;

Query Match 15.4%; Score 159.5; DB 8; Length 188;

[illegible]

Search completed: January 9, 2006, 15:30:27
Job time : 88.515 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 9, 2006, 15:25:12 ; Search time 25.423 Seconds
(without alignments)
614.628 Million cell updates/sec

Title: US-09-811-367b-1

Perfect score: 1023

Sequence: 1 MTDSVITYSMLEPTATQAQN.....GLQSSCEVPLHGCKKRL 189

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 991

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCrus_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.5	51.4	188	2	US-08-722-126A-5
2	525.5	51.4	188	4	PCT-US95-04258-5
3	55	5.4	188	1	US-08-486-715-5
4	55	5.4	188	1	US-08-486-715-5
5	55	5.4	188	1	US-08-476-100-5
6	55	5.4	188	1	US-08-286-767-3
7	55	5.4	188	2	US-08-475-749-5
8	54.5	5.3	188	2	US-10-104-047-2380
9	53.5	5.2	188	2	US-09-328-352-7291
10	52	5.1	188	2	US-09-122-443-14
11	52	5.1	188	2	US-09-558-089-14
12	52	5.1	188	2	US-09-558-087-14
13	52	5.1	188	2	US-09-558-474-14
14	52	5.1	188	2	US-09-123-482A-1
15	50.5	4.9	188	2	US-09-543-681A-7232
16	50	4.9	189	2	US-09-489-039A-9728
17	48.5	4.7	188	2	US-07-757-022B-32
18	48	4.7	189	2	US-09-270-767-36523
19	48	4.7	189	2	US-09-270-767-51740
20	47	4.6	189	2	US-09-206-935-19
21	47	4.6	189	2	US-09-206-936-19
22	47	4.6	189	2	US-07-145-002B-12
23	47	4.6	189	2	US-07-145-002B-22
24	47	4.6	189	2	US-06-256-204C-12
25	47	4.6	189	2	US-06-256-204C-22
26	47	4.6	189	2	US-09-919-497-73
27	46	4.5	188	2	US-09-248-796A-23410

28	46	4.5	189	2	US-09-487-792-8	Sequence 8, Appl
29	46	4.5	189	2	US-09-322-409-111	Sequence 11, App
30	46	4.5	189	2	US-09-908-594-8	Sequence 8, Appl
31	46	4.5	189	2	US-09-451-527-111	Sequence 11, App
32	46	4.5	189	2	US-09-198-452A-1169	Sequence 1169, App
33	45.5	4.4	189	2	US-09-303-518D-232	Sequence 232, App
34	44.5	4.4	189	1	US-08-026-758-16	Sequence 16, Appl
35	44	4.3	188	2	US-09-252-991A-20399	Sequence 20399, A
36	44	4.3	188	2	US-09-270-767-37708	Sequence 37708, A
37	44	4.3	188	2	US-09-270-767-52925	Sequence 52925, A
38	44	4.3	189	2	US-09-451-527-168	Sequence 168, App
39	43.5	4.3	189	1	US-08-026-758-17	Sequence 17, Appl
40	43.5	4.3	189	2	US-09-487-792-7	Sequence 7, Appl
41	43.5	4.3	189	2	US-09-908-594-7	Sequence 7, Appl
42	43.5	4.3	189	2	US-09-902-540-14285	Sequence 14285, A
43	43	4.2	188	2	US-09-252-991A-29853	Sequence 29853, A
44	43	4.2	188	2	US-09-252-991A-31741	Sequence 31741, A
45	43	4.2	188	2	US-09-527-376-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-722-126A-5
Sequence 5, Application US/08722126A
Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: UNITED STATES OF AMERICA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-5
Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 1.7e+48;

	Matches	100; Conservative	29; Mismatches	57; Indels	1; Gaps	1
Qy	1	MTDSVITYMELPTPTQANDYGPQOKSSSKRPSCLVAITLGLITLAVLSVLLYOMIL				60
Db	1	MADNSIYETLELPAPPRVQDSDRMVKYKVLHPRCVSLVMVALGLITVILMSLLTYORTL				60
Qy	61	CGGSNYSTFCASCPSPCDRMKKYKGNHCYFYSVEKDNMSLEFCLARDSHLVTITDNOEMS				120
Db	61	CCGSIGGFMCSQSCSRCPNLIMRMRGSHICYTSMKRDMSLTKRCADKGSHTLTFPPDQGVN				120
Qy	121	LLQVFLSAFCWIGLRNNSGMRWEDGSPINFSRISNSFVQTGAIINXNGILQASSCEVPL				180
Db	121	LFOEVAGDEDFWIGLRIDIDGMRWEDGPAISLS-ILSNSVQCGCTIHRGCLHAASCEVAL				179
Qy	181	HGVCKKV				187
Db	180	QWICEKV				186

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RESULT 2
PCT-US95-04258-5
; Sequence 5, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECTH=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04258-5

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Query Match	51.4%	Score 525.5	DB 4	Length 188
Best Local Similarity	53.5%	Pred. No. 1.7e-48		
Matches 100; Conservative	29;	Mismatches 57;		Indels 1; Gaps 1

Qy 1 MTD5IY5M5LEPTTQAO5ND5G5POOK5SS5R5P5SC5CA5I5R5GL5T5A5L5V5I5Y5OM5L 60

Db 1 MADNSI5T5LE5LP5A5P5R5VO5DB5R5M5K5Y5K5A5V5I5H5P5C5I5Y5L5M5A5G5I5T5I5M5B5L5Y5O5R5L 60

Qy 61 CQGSNY5T5C5A5C5P5C5P5D5R5M5K5Y5G5H5C5Y5F5V5E5K5O5N5S5L5E5F5C5L5A5R5D5H5L5I5V5T5D5Q5M5 120

Db 61 CCGSG5G5F5M5C5Q5C5R5P5D5L5M5R5G5H5C5Y5F5M5K5R5D5N5S5L5K5C5A5G5S5I5L5F5P5P5N5O5G5N 120

Qy	121	LILVFLSEAFICIGLRNNSGMRMEGSPLTNSRSLSSNSFVOTCGAIVKNGGLQASSCEVPL	180
	:	:::::	:
	:	:::::	:
	:	:::::	:
Db	121	LPEYVGEFGFYIIGLRIDSGRMEDGPALSLIS-ILSNSVVGKCTIHRCGGHMSSCVAL	179
	:	:	:
Qy	181	HGVCKKV	187
	:	:	:
	:	:	:
Db	180	QMICEKV	186

US-08-486-715-5
 Sequence 5, Application US/08486715
 Patent No. 5674724
 GENERAL INFORMATION:
 APPLICANT: Miller, Samuel I.
 TITLE OF INVENTION: SALMONELLA VIRULENCE GENES
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Fish & Richardson P. C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: Wordperfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,715
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/090,526
 FILING DATE: 09-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/629,602
 FILING DATE: 18-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00786/192005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 JS-08-486-715-5

Query Match 5.4%; Score 55; DB 1; Length 188;
Best Local Similarity 35.8%; Pred. No. 6.4e+02;
Matches 14; Conservative 9; Mismatches 9; Indels 6; Gaps 2

RESULT 4 719-5
US-08-486-719-5
; Sequence 5, Application US/08486719
; Patent No. 5674736
; GENERAL INFORMATION:
; APPLICANT: Miller, Samuel I.
; TITLE OF INVENTION: SALMONELLA VIRULENCE GENES
; NUMBER OF SEQUENCES: 5


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MOLECULE TYPE: protein
US-08-286-767-3

Query Match      5.4%; Score 55; DB 1; Length 188;
Best Local Similarity 36.8%; Pred. No. 6.4e+02;
Matches 14; Conservative 9; Mismatches 9; Indels 6; Gaps 2;

QY 138 NSGWRMEDGSPINRSISSNFV---QTGAIKNGKL 171
Db      50 NVKRYEDDSPVSF--ISSLSYLGRDQAGSVEPEGI 85

US-08-475-749-5
Sequence 5, Application US/08475749
Patent No. 6010901
GENERAL INFORMATION:
APPLICANT: Miller III, Samuel I.
APPLICANT: Melanos, John L.
TITLE OF INVENTION: SALMONELLA VIRULENCE GENES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P. C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475, 749
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,526
FILING DATE: 09-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/629,602
FILING DATE: 18-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/192004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-749-5

Query Match      5.4%; Score 55; DB 2; Length 188;
Best Local Similarity 36.8%; Pred. No. 6.4e+02;
Matches 14; Conservative 9; Mismatches 9; Indels 6; Gaps 2;

QY 138 NSGWRMEDGSPINRSISSNFV---QTGAIKNGKL 171
Db      50 NVKRYEDDSPVSF--ISSLSYLGRDQAGSVEPEGI 85

RESULT 8
US-10-104-047-2380
Sequence 2380, Application US/10104047
Patent No. 6943241

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2380
LENGTH: 188
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-2380

Query Match      5.3%; Score 54.5; DB 2; Length 188;
Best Local Similarity 23.0%; Pred. No. 7.3e+02;
Matches 38; Conservative 18; Mismatches 46; Indels 63; Gaps 11;

QY 51 LSVLLYQWILCOG-----SNYSTGASCPCSPDRMKYGHCHYFVSVEKMNLSLECL 104
Db      35 LTYLLYRWE--QGSGGSHQWYTA-----NRQWNGS-----DPLIGSHSWCD 77

QY 105 ARDS--HLVITDNEMLLVFLSEARCWIGLRNNGWR-----MED 145
Db      78 CGSSFPFH-----GLAISLSE-WTMWG-KPSSWMAAGIKSIGLARRRACGWT 125

QY 146 GSP-----INFSRISSNFVQTCG--AINKNGIQASCEVPLH 181
Db      126 GMRGSSPGSLPNSNRLSLVPLVPSASMTLRMSRPASSCTTALLY 170

RESULT 9
US-09-328-352-7291
Sequence 7291, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7291
LENGTH: 188
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7291

Query Match      5.2%; Score 53.5; DB 2; Length 188;
Best Local Similarity 39.5%; Pred. No. 9.3e+02;
Matches 15; Conservative 3; Mismatches 17; Indels 3; Gaps 1;

QY 100 IEFCLARDSHLIVITDNEMSLLQVFLSEAPCWIGLRN 137
Db      28 LSYCLAMDHLHQFLPNKEPSSIQWF---PFWISQVN 62

RESULT 10
US-09-122-443-14
Sequence 14, Application US/09122443
Patent No. 6060284
GENERAL INFORMATION:
APPLICANT: Bazar, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE, RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California

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COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,443
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-122-443-14

Query Match 5.1%; Score 52; DB 2; Length 188;
Best Local Similarity 20.5%; Pred. No. 1.4e+03;
Matches 27; Conservative 17; Mismatches 54; Indels 34; Gaps 3;

QY 44 GLTAVLISLVLYQWILCOGSN-----YSTCASCPCSC--- 75
DB 30 GLITHLMEIVEMRKELCNGNSDCMNNDDALAENNLKLPFIQRNDGCTGYNOEICLK 89
QY 76 -PDRMKYGNHCYFVSVEKDNSSLEFCLARDSHLVITDNOEMS-----LIQVFLSEA 129
DB 90 ISSGLLEHYSHYLEMKNLKDKNKDKARVLRDTETLIHFNOEVKDLHKIVLPTPIISNA 149
QY 130 FCWIGLRNNSGW 141
DB 150 LITDKLESQKEM 161

RESULT 11
US-09-558-089-14
Sequence 14, Application US/09558089
Patent No. 6479634
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE, RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,089
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/122,443

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-558-089-14

Query Match 5.1%; Score 52; DB 2; Length 188;
Best Local Similarity 20.5%; Pred. No. 1.4e+03;
Matches 27; Conservative 17; Mismatches 54; Indels 34; Gaps 3;

QY 44 GLTAVLISLVLYQWILCOGSN-----YSTCASCPCSC--- 75
DB 30 GLITHLMEIVEMRKELCNGNSDCMNNDDALAENNLKLPFIQRNDGCTGYNOEICLK 89
QY 76 -PDRMKYGNHCYFVSVEKDNSSLEFCLARDSHLVITDNOEMS-----LIQVFLSEA 129
DB 90 ISSGLLEHYSHYLEMKNLKDKNKDKARVLRDTETLIHFNOEVKDLHKIVLPTPIISNA 149
QY 130 FCWIGLRNNSGW 141
DB 150 LITDKLESQKEM 161

RESULT 12
US-09-558-087-14
Sequence 14, Application US/09558087
Patent No. 6495667
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE, RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558,087
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid

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; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14
US-09-558-087-14

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Query Match	5.1%;	Score 52;	DB 2;	Length 188;
Best Local Similarity	20.5%;	Pred. No. 1.4e+03;		
Matches 27;	Conservative 17;	Mismatches 54;	Indels 34;	Gaps 3

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QY      44 GLLTAVLLSVLTLQWILLCOGSN-----YSTASCPSC---75
Db      30 GLITHTVLMEIVEMRKELCNGNSDCMNDNALANNILKLPEIQNDGGCYGTGNGEITLKL 89

QY      76 -PDRMKYNGCHCYFFVEEEKDMNMSLEFCLARDSHLYITNDQEMS-----LQVFLSEA 129
Db      90 ISSGLLEFHYSLIYEMKANKLKDKKKAKARLYQDRTLTHIFQGVKDLKIVLEPPIISNA 149

QY      130 FCWIGLRNNSGW 141
Db      150 LLTDTKLESQKEW 161

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RESULT 13
US-09-558-474-14
; Sequence 14, Application US/09558474
; Patent No. 6835825

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1  APPLICANT: Bazan, J. Fernando
2  TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
3  NUMBER OF SEQUENCES: 16
4  CORRESPONDENCE ADDRESS:
5
6
7
8
9
10
11
12
13
14
15
16
17
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21
22
23
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STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:

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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/558.474
? FILING DATE: 25-Apr-2000
? CLASSIFICATION: <Unknown>

```

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/053,765
 ; FILING DATE: 25-JUL-1997
 ; ATTORNEY/AGENT INFORMATION:
 ;

1 NAME: CHING, EDWIN P.
2 REGISTRATION NUMBER: 34,090
3 REFERENCE/DOCKET NUMBER: DX075841
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (650) 852-9196
6 TELEFAX: (650) 496-1200
7 INFORMATION FOR SEQ ID NO: 14:
8 SEQUENCE CHARACTERISTICS:
9

```

; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14
IS-09-558-474-14

```

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Query March          5.1%; Score 52; DB 2; Length 188;  
Best Local Similarity 20.5%; Pred. No. 1.4e+03;  
Matches 27; Conservative 17; Mismatches 54; Indels 34; Gaps 3  
  
OY      44 GLTRPVLLSVLLVQMLTGGSN-----YSTCASCSPC--- 75  
||:|||::: ||:::
```

Db 30 GLTHTLWMIYEMRKELCNGSDCMANDDALENNLKLPETORDGCVOTGVNOEICLLK 89

Qy 76 -PDRMKYCNHCYFSEVEEKDWNSSLFECLARDSHLIVITNOEMS-----LLQVFLSEA 129

Db 90 ISSGGLLEHYSYLEWMKNMLKQKKQKAVLRQDFTTLIHINQGVKDLHKLVLETPISNA 149

Qy 130 FCWIGLGRNNSGW 141

Db 150 LLTDLKLESQKEW 161

RESULT 14
US-09-123-492A-1
; Sequence 1, Application US/09123492A
Date: 01/07/00

```

1  TITLE OF INVENTION: METHOD FOR EVALUATING AND AFFECTING MALE FERTILITY
2  FILE REFERENCE: KLINEPETER-1B
3  CURRENT APPLICATION NUMBER: US/09/123,452A
4  CURRENT FILING DATE: 1998-07-28
5  PRIOR APPLICATION NUMBER: 08/593,677
6  PRIOR FILING DATE: 1997-01-29
7  PRIOR APPLICATION NUMBER: PCT/US97/01725
8  PRIOR FILING DATE: 1997-01-29
9  PRIOR APPLICATION NUMBER: 60/082,753
10 PRIOR FILING DATE: 1998-04-23
11 NUMBER OF SEQ ID NOS: 6
12 SOFTWARE: PatentIn Ver. 2.0
13 SEQ ID NO 1
14 LENGTH: 189
15 TYPE: PRT
16 ORGANISM: Human DJ-1
17 US-09-123-492A-1

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Query Match	5.1%	Score 52;	DB 2;	Length 189;
Best Local Similarity	31.9%;	Pred. No. 1.4e+03;		
Matches 23; Conservative	9;	Mismatches 26;	Indels 14;	Gaps 4

```
QY      44 GLTAVLL--SVLLYQMILCOGSNNTCSACSPSCDPDRMMKGNHCYFVSVEEDW----- 96
          || : | : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db     100 GLIAICAGPTALLAHEIG-GSKVTT---HPLAKDKMNGGHYYTSENRVEDGLIITS 155
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QY      97 ---NSSLEFCLA 105
      : | | | |
Db      156 RGPSTFEFALA 167
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RESULT 15
US-09-543-681A-7232
; Sequence 7232, Application US/09543681A

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? APPLICANT: GARY BRETON
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
? TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: 2709.1002-001
? CURRENT APPLICATION NUMBER: US/09/543,681A
? CURRENT FILING DATE: 2000-04-05
? PRIOR APPLICATION NUMBER: US 60/128,706
? PRIOR FILING DATE: 1999-04-09
? NUMBER OF SEQ ID NOS: 8344
? SEQ ID NO 7232
? LENGTH: 188
? TYPE: PRT
? ORGANISM: Proteus mirabilis
? US-09-543-681A-7232

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Query Match	4.9%	Score 50.5;	DB 2,	length 188;
Best Local Similarity	21.0%;	Pred. No. 2e+03;		
Matches 30;	Conservative 16;	Mismatches 56;	Indels 41;	Gaps 8
15 ATGAGNDYGPQRSSSKPSCSCVATITGTTAVLVSVLXQWILCGGSNNSTC-----	69			

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Db      50 ALKSQGD-GOVIKYLEGQP-COCCGA-----DLVLRQKFGMFIGC--SNYPACEHIEQ 99
QY      70 -----ASCPECP-----DRMKYGNHCY-----YFSVEEKWNSSLEFCLARDS 108
Db      100 IDKPDETVHCFQCEKSKLQKRSRFGKIFYACNOYFECQFVUNNKPINGECEYC----- 154
QY      109 HLLVITDNOEMSLQVFLSEAPC 131
Db      155 HYLIMEKRSSQGVRLVCASKLC 177
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Search completed: January 9, 2006, 15:37:59
Job time : 26.423 sec8

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Page 10

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 14:41:26 ; Search time 87.977 Seconds
(without alignments)
943.913 Million cell updates/sec

Title: US-09-811-367b-1

Sequence: 1 MTDSYIYSMLLPATQAQN.....GLQASSCEVPHGCKKVEL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 6014

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003s:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	100.0	189	2	AAW88265
2	1023	100.0	189	4	AAE11759
3	1007	98.4	189	7	ADD25635
4	1007	98.4	189	9	ADY19892
5	548.5	53.6	188	4	AAE11760
6	525.5	51.4	188	2	AAW88277
7	525.5	51.4	188	2	AAW88277
8	525.5	51.4	188	4	AAE11761
9	168.5	16.5	189	9	AEA89021
10	165	16.1	189	4	AAU19837
11	165	16.1	189	4	ABH17910
12	165	16.1	189	5	ABP48057
13	165	16.1	189	7	ADCL1019
14	159	15.5	188	4	AAW78675
15	159	15.5	188	4	AAU06671
16	159	15.5	188	6	ABO32533
17	159	15.5	188	7	ADP65310
18	159	15.5	188	8	ADQ10144
19	159	15.5	188	8	ADP25141
20	103.5	10.1	188	4	ABBS5966
21	100.5	9.8	189	7	ADCC3690
22	92.5	9.0	189	8	ADN22989
23	87.5	8.6	189	9	ABW70262
24	72.5	7.1	188	4	ABBS5823

25	66.5	6.5	189	5	ABP06929	Abp06929 Human ORF
26	59	5.8	188	3	AA60460	AA60460 Arabidops
27	59	5.8	188	3	AA60561	AA60561 Arabidops
28	57	5.6	189	8	ADK77191	ADK77191 Plant full
29	57	5.6	189	8	ADK67118	ADK67118 Plant full
30	55.5	5.4	189	8	ADK10104	ADK10104 Human pro
31	55	5.4	189	8	AAK26415	AAK26415 pagC/AP f
32	55	5.4	188	2	AAK26415	AAK26415 pagC. 3/2
33	55	5.4	188	2	AAK70744	AAK70744 pagC prot
34	55	5.4	188	2	AAK70744	AAK70744 S. typhim
35	55	5.4	188	2	AAK18380	AAK18380 S. typhim
36	55	5.4	188	6	ABP88198	ABP88198 Amino acil
37	54.5	5.3	189	6	ABP58704	ABP58704 Human sod
38	54.5	5.3	188	7	AAK35627	AAK35627 Arabidops
39	53.5	5.2	188	6	ADK36004	ADK36004 Acinetoba
40	53.5	5.2	189	3	AAK33435	AAK33435 Zea mays
41	53	5.2	188	3	AAK33865	AAK33865 HPV16 B6/
42	52.5	5.1	188	8	ADY24659	ADY24659 Plant full
43	52	5.1	188	2	AAW95013	AAW95013 Mouse int
44	52	5.1	188	9	ADY98163	ADY98163 Mouse int
45	52	5.1	188	9	ABK47343	ABK47343 Mouse int

ALIGNMENTS

RESULT 1	AAW88265	standard; protein; 189 AA.
ID	AAW88265	
XX	AAW88265:	
AC		
XX		
DT	29-MAR-1999	(first entry)
XX		
DE	Human mast cell function-associated antigen (MAFA).	
XX		
KW	Mast cell function-associated antigen; MAFA; splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	7..10
FT	Modified-site	/note="ITIM motif"
FT	Modified-site	65..67
FT	Modified-site	/note="Asn is N-glycosylated"
FT	Modified-site	97..99
FT	Modified-site	/note="Asn is N-glycosylated"
FT	Modified-site	137..139
FT	Modified-site	/note="Asn is N-glycosylated"
FT	Modified-site	150..152
FT	Modified-site	/note="Asn is N-glycosylated"
XX	WO9854209-A2.	
XX		
PD	03-DEC-1998.	
XX		
XX	29-MAY-1998;	98MO-GB001572.
XX		
PR	31-MAY-1997;	97GB-00011148.
XX		
PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.	
XX		
PI	Hewitt EL, Lamers MBAC, Lamont A, Williams DH,	
XX		
DR	WPI; 1999-059806/05.	
XX	N-PSDB; AAV84198.	
XX		
PT	New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.	
PT		
XX		

PS Disclosure; Fig 1; 44pp; English.

CC This is the amino acid sequence of human mast cell function- associated
CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAW84198)
CC encoding human MAFA can be obtained from myelogenous leukemic cell line
CC KU812 or cDNA derived from human lung tissue. The encoded protein is
CC similar to the rat form (see AAW8277) having an intracellular domain
CC containing a putative immunoreceptor tyrosine activation motif (ITIM) and
CC an extracellular lectin-like domain. 2 Alternatively spliced forms (see
CC AAW8266-67) of human MAFA have been identified. Polypeptides and
CC synthetic peptides (see AAW8258-64) based on these truncated MAFA
CC proteins can be used in methods for the treatment of inflammatory and
CC allergic diseases, and tumour growth

CC Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 2.7e-98;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVYISMLLPRTAQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60
DB 1 MTDVYISMLLPRTAQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60
QY 61 CGSNVSTCASCPCSPDRMKYGNHCYFSEBKMNSLFECLARDSHLVTITNOEMS 120
DB 61 CGSNVSTCASCPCSPDRMKYGNHCYFSEBKMNSLFECLARDSHLVTITNOEMS 120
QY 121 LLOVFLSEAFQWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
DB 121 LLOVFLSEAFQWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HGVCCKVRL 189

RESULT 2

AAE11759
ID AAE11759 standard; protein; 189 AA.

AC AAE11759;

DT 18-DEC-2001 (first entry)

DE Human mast cell function associated antigen (MAFA) protein.

KW Human; pharmaceutical composition; mast cell function associated antigen;
KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KW immunosuppressive; cytostatic.

XX Homo sapiens.

XX WO200170805-A2.

XX 27-SEP-2001.

XX 16-MAR-2001; 2001WO-US008596.

XX 17-MAR-2000; 2000US-0190716P.

XX (GEMI-) GEMINI SCI INC.

XX Takahashi N, Mikayama T;

XX WPI; 2001-611482/70.

XX N-PSDB; AAD18734.

PT Pharmaceutical composition for treating tumor by stimulating cytotoxic
PT activity of natural killer cell or T-cell, comprises an agent that binds
PT to mast cell function-associated antigen ligand on target cell.

PS Claim 10; Page 18; 49pp; English.

XX The present invention relates to a pharmaceutical composition comprising
CC an agent which specifically binds to a mast cell function associated
CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
CC ligand and a pharmaceutically acceptable excipient. The invention is
CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
CC binding to a ligand on a target cell, by contacting the pharmaceutical
CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is human MAFA protein

XX Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 2.7e-98;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVYISMLLPRTAQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60
DB 1 MTDVYISMLLPRTAQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60
QY 61 CGSNVSTCASCPCSPDRMKYGNHCYFSEBKMNSLFECLARDSHLVTITNOEMS 120
DB 61 CGSNVSTCASCPCSPDRMKYGNHCYFSEBKMNSLFECLARDSHLVTITNOEMS 120
QY 121 LLOVFLSEAFQWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
DB 121 LLOVFLSEAFQWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HGVCCKVRL 189

RESULT 3

ADD25635
ID ADD25635 standard; protein; 189 AA.

AC ADD25635;

DT 15-JAN-2004 (first entry)

DE Binding domain-immunoglobulin fusion protein-associated protein #95.

KW Binding domain; immunoglobulin; fusion protein; cytostratic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neutroprotective; hinge region; immunoglobulin heavy chain;

KW CH2 constant region; CH3 constant region; 19G1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX Unidentified.

XX US2003118592-A1.

XX 26-JUN-2003.

XX 25-JUN-2002; 2002US-00207655.

XX 17-JAN-2001; 2001US-0367358P.

XX 17-JAN-2002; 2002US-00053530.

XX 03-JUN-2002; 2002US-0385691P.

XX (GENE-) GENECRAFT INC.

PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
XX WPI; 2003-801317/75.
XX

PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
XX

PS Disclosure; SEQ ID NO 196; 157bp; English.

XX The invention relates to a binding domain-immunoglobulin fusion protein
XX comprising a binding domain polypeptide that is fused to an
XX immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
XX CH2 constant region polypeptide that is fused to the hinge region
XX polypeptide, and an immunoglobulin heavy chain CH3 constant region
XX polypeptide that is fused to the CH2 constant region polypeptide. The
XX hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin
XX hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
XX region polypeptide; derived from (a) having 3 or more cysteine residues;
XX where the mutated human IgG1 immunoglobulin hinge region polypeptide
XX contains 2 cysteine residues, where the first cysteine is not mutated; a
XX mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
XX (a) having 3 or more cysteine residues, where the mutated human IgG1
XX immunoglobulin hinge region polypeptide contains no more than one
XX cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
XX polypeptide, derived from (a) having 3 or more cysteine residues; where
XX the mutated human IgG1 immunoglobulin hinge region polypeptide contains
XX no cysteine residues. The binding domain-immunoglobulin fusion protein is
XX capable of at least one immunological activity comprising antibody
XX dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
XX binding domain polypeptide is capable of specifically binding to an
XX antigen. Also included are an isolated polynucleotide encoding the
XX binding domain-immunoglobulin fusion protein, a recombinant expression
XX construct comprising the polynucleotide (operably linked to a promoter),
XX a host cell transformed or transfected with a recombinant expression
XX construct, producing the binding domain-immunoglobulin fusion protein, a
XX pharmaceutical composition comprising the binding domain-immunoglobulin
XX fusion protein or polynucleotide and a carrier, and treating a subject
XX having or suspected of having a malignant condition or a B-cell disorder.
XX The binding domain-immunoglobulin fusion protein is useful for treating a
XX subject having or suspected of having a malignant condition or a B-cell
XX disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
XX myasthenia gravis, Grave's disease, type 1 diabetes mellitus, multiple
XX sclerosis or autoimmune disease. The present sequence is a binding domain
XX -immunoglobulin fusion protein-associated protein sequence. Note: The
XX sequence data for this patent formed part of the printed specification
XX and is also available in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not
XX identified the sequences in the printed specification by their SEQ ID
XX number therefore none of the sequences can be explicitly identified.

XX Sequence 189 AA:

Query Match 98.4%; Score 1007; DB 7; Length 189;

Best Local Similarity 98.4%; Pred. No. 1.3e-96;

Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVITSMLELPTAQAQNDYGPQKSSSKPSCGLVAITLGLTAVLLSVLYQWIL 60
DB 1 MTDVITSMLELPTAQAQNDYGPQKSSSKPSCGLVAITLGLTAVLLSVLYQWIL 60
QY 61 CQGSNVTSCASCPCPRMVKYGNHCYFVSVEEDKNNSLFCLARDSHLLVITDNOEMS 120
DB 61 CQGSNVTSCASCPCPRMVKYGNHCYFVSVEEDKNNSLFCLARDSHLLVITDNOEMS 120
QY 121 LLQVFLSEAFQWIGLRNNSGWRWEDGSPINFSSISNFVQTGCAINKNGLQASSCEVPL 180
DB 121 LLQVFLSEAFQWIGLRNNSGWRWEDGSPINFSSISNFVQTGCAINKNGLQASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HWCKCKVRL 189

RESULT 4
ADY19892
ID ADY19892 standard; protein; 189 AA.

XX
XX AC ADY19892;
XX

DT 05-MAY-2005 (first entry)

XX PRO polypeptide SEQ ID NO 5698.

XX Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
XX Antithyroid; Antidiabetic; Nephroretropic; CNS-Gen.; Hepatocretropic;
XX Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiaesthetic;
XX Antiallergic; diagnosis.

XX Homo sapiens.

XX MO2005016962-A2.

XX 24-FEB-2005.

XX 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

XX (GENTH) GENENTECH INC.

PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating an immune related disorder, e.g. systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

XX Claim 8; SEQ ID NO 5698; 158bp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. The polypeptide, agonist or an antagonist, antibody,
XX composition, and method are useful for diagnosing and treating an immune
XX related disorder, e.g. systemic lupus erythematosus, rheumatoid
XX arthritis. The present sequence represents a PRO polypeptide.

XX Sequence 189 AA:

Query Match 98.4%; Score 1007; DB 9; Length 189;

Best Local Similarity 98.4%; Pred. No. 1.3e-96;

Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVITSMLELPTAQAQNDYGPQKSSSKPSCGLVAITLGLTAVLLSVLYQWIL 60
DB 1 MTDVITSMLELPTAQAQNDYGPQKSSSKPSCGLVAITLGLTAVLLSVLYQWIL 60
QY 61 CQGSNVTSCASCPCPRMVKYGNHCYFVSVEEDKNNSLFCLARDSHLLVITDNOEMS 120
DB 61 CQGSNVTSCASCPCPRMVKYGNHCYFVSVEEDKNNSLFCLARDSHLLVITDNOEMS 120
QY 121 LLQVFLSEAFQWIGLRNNSGWRWEDGSPINFSSISNFVQTGCAINKNGLQASSCEVPL 180
DB 121 LLQVFLSEAFQWIGLRNNSGWRWEDGSPINFSSISNFVQTGCAINKNGLQASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HWCKCKVRL 189
RESULT 5
AAE11760
ID AAE11760 standard; protein; 188 AA.
XX
XX AAE11760;

```

XX 18-DEC-2001 (first entry)
DT Mouse mast cell function associated antigen (MAFA) protein.
DE
XX
XX Mouse; pharmaceutical composition; mast cell function associated antigen;
XX MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
XX immunosuppressive; cytostatic.
XX
OS Mus sp.
XX
XX Key Location/Qualifiers
XX FH 64..188
XX FT Domain /note="Extracellular domain"
XX
XX WO200170805-A2.
XX
XX 27-SEP-2001.
XX
XX 16-MAR-2001; 2001WO-US008596.
XX
XX 17-MAR-2000; 2000US-0190716P.
XX
XX (GEMI-) GEMINI SCT INC.
XX
XX Takehashi N, Miyayama T;
XX
XX MPI: 2001-611482/70.
XX
XX N-PSDB; MAD18735.
XX
XX Pharmaceutical composition for treating tumor by stimulating cytotoxic
XX activity of natural killer cell or T-cell, comprises an agent that binds
XX to mast cell function-associated antigen ligand on target cell.
XX
XX Example 1; Page 19; 49pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
XX an agent which specifically binds to a mast cell function associated
XX antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
XX killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA
XX ligand and a pharmaceutically acceptable excipient. The invention is
XX useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
XX binding to a ligand on a target cell, by contacting the pharmaceutical
XX composition in vitro, ex vivo or in vivo by administering the composition
XX to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
XX an amount sufficient to inhibit cell surface MAFA binding to the ligand
XX on the target cell. The agent or the composition is useful for treating a
XX tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
XX T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
XX tumour cell. The invention is also useful for inhibiting an activity of
XX NK cell or a T-cell. The present sequence is mouse MAFA protein
XX
SQ Sequence 188 AA;
Query Match 53.6%; Score 548.5; DB 4; Length 188;
Best Local Similarity 55.6%; Pred. No. 16-48;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
QY 1 MTDSTVYMLLEPTATQANDYGPQOKSSSKPSCGLVATITGLTAVLSVLLYQMTL 60
DB 1 MADSTVSTLELPAAPRVQDDSRWKVKAHLRPHLSRFAMVALGLTIVILMSLTYORTL 60
QY 61 CGGSNYSTCASCPCSPDRMKYGNHCYFSEYBEKDMNSLBEFLARDSHLVTITDNOEMS 120
DB 61 CGGSNDSTCSHCPSCPILMTNRGSHCYFSEMEKDMNSLKFCDKGSHTLTFPNDGYNK 120
QY 121 LLOVFLSEAFQWIGLRNNSGMRWEDGSPLNFSRISNSFVQTGAINKXGLQASSCEVPL 180
DB 121 LFGELYGDFYWIGLRNIDGMRWEGPALSL-RILTNLSIQCGAIIHRNGLQASSCEVAL 179
QY 181 HGVCKKV 187
DB 180 QWICKKV 186

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RESULT 6
AAR77033
ID AAR77033 standard; protein, 188 AA.
XX
XX AAR77033;
XX
XX 01-FEB-1996 (first entry)
XX
XX Mammalian mast cell function-associated antigen (MAFA).
XX
XX Mast cell function-associated antigen; MAFA; soluble; ligand;
XX identification; screening; inflammation; inflammatory; allergy; allergic;
XX prevention.
XX
XX Rattus rattus.
XX
XX WO9527734-A1.
XX
XX 19-OCT-1995.
XX
XX 06-APR-1995; 95WO-US004258.
XX
XX 08-APR-1994; 94IL-00109257.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX (RYCVU) RYCUS A.
XX
XX Pecht I, Gutmann MD, Tal M;
XX
XX MPI: 1995-366356/47.
XX
XX N-PSDB; AAT01471.
XX
XX Novel DNA encoding a mast cell function-associated antigen (MAFA) -
XX useful for screening for ligands of MAFA which are useful for prevention
XX of inflammatory and allergic reactions.
XX
XX Claim 12; Page 37; 54pp; English.
XX
XX A soluble form of mast cell function-associated antigen (MAFA) can be
XX produced by recombinant techniques for use in the ligand- screening
XX assay. The ligands that are identified may be used alone or in
XX combination with the MAFA to prevent inflammatory and allergic reactions
XX
SQ Sequence 188 AA;
Query Match 51.4%; Score 525.5; DB 2; Length 188;
Best Local Similarity 53.5%; Pred. No. 2.5e-46;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
QY 1 MTDSTVYMLLEPTATQANDYGPQOKSSSKPSCGLVATITGLTAVLSVLLYQMTL 60
DB 1 MADNSTVSTLELPAAPRVQDDSRWKVKAHLRPHLSRFAMVALGLTIVILMSLTYORTL 60
QY 61 CGGSNYSTCASCPCSPDRMKYGNHCYFSEYBEKDMNSLBEFLARDSHLVTITDNOEMS 120
DB 61 CGSGKGFMCQCSRCRPNLMMNNGSHCYFSEMEKDMNSLKFCDKGSHTLTFPNDGYNV 120
QY 121 LLOVFLSEAFQWIGLRNNSGMRWEDGSPLNFSRISNSFVQTGAINKXGLQASSCEVPL 180
DB 121 LFOEYVGEDFYWIGLRNIDGMRWEDGPAISLS-IISNSVVOKCGTIRHCGLHASSCEVAL 179
QY 181 HGVCKKV 187
DB 180 QWICKKV 186

```

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RESULT 7
AAM88277
ID AAM88277 standard; protein, 188 AA.
XX
XX AAM88277;

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```
RESULT 9
AEA89021
ID AEA89021 standard; protein; 188 AA.
XX
AC AEA89021;
XX
DT 25-AUG-2005 (first entry)
XX
DE Chicken MHC C-type lectin receptor, B-1ec protein.
XX
KW Transgenic animal; disease-resistance; gene therapy; screening; B-1ec;
KW lectin; major histocompatibility complex; receptor.
XX
OS Gallus gallus.
XX
PN WO2005054280-A2.
XX
PD 16-JUN-2005.
XX
PF 03-DEC-2004; 2004WO-GB005108.
XX
PR 05-DEC-2003; 2003GB-00028248.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI (ANIM-) INST ANIMAL HEALTH.
XX
PI Carrol1 M, Kaufman J, Mitrophanous K;
XX
DR WPI; 2005-425385/43.
XX
DR N-PSDB; AEA89020.
XX
PT Producing transgenic animal having modified resistance to disease, by
PT introducing retrovirus having polynucleotide sequence encoding protein
PI that modifies disease resistance of animal, into cell of animal.
XX
PS Disclosure; SEQ ID NO 8; 90pp; English.
XX
XX
XX The present invention relates to a method of producing transgenic animal
XX having modified resistance to a disease. The method involves introducing
XX retrovirus having polynucleotide sequence encoding protein that modifies
XX disease resistance of animal, into cell of animal. The invention is
XX useful for screening proteins capable of modifying resistance of an
XX animal to a disease, for producing transgenic bird and fish and also
XX useful in gene therapy. The present sequence is the chicken major
XX histocompatibility complex (MHC) C-type lectin receptor, B-1ec protein.
XX This sequence is used to produce a transgenic animal having modified
XX resistance to a disease.
XX
XX
XX Sequence 188 AA;
SQ
Query Match 16.5%; Score 168.5; DB 9; Length 188;
Beet Local Similarity 27.3%; Pred. No. 5e-09; Indels 27; Gaps 6;
Matches 48; Conservative 24; Mismatches 77;
QY 26 QKSSSKSPSC-----SCLVAITLGLTAVLTLVLYOWILCOGSNYSTCASCPSPDRWM 80
DB 17 RREGSPRGACVTFQULTMAVFTVLITNAFAVQAFQ-----PHQPCAQCFPMWI 67
QY 81 KYGNHCYFVSVEKCMNSSLFECCLARDSHLVTITNQEMSLQVFLSEAFCTIGLRNNS- 139
DB 68 GFRGCKCYFSEDESSQNNCSALGASLAVFDSAEIDLSFTMRHKGSSPHWVGLSREGK 127
QY 140 ---GAWWEDGSLNFRISNSF-VQ---TCGAINKNGLOASCEVPLHGVCKKVL 189
DB 128 EHPWEMVNRSP-----SHLFQVQGDGLCAVLGAGLSSSHCSARRMVCTKPAL 177
RESULT 10
AAU19837
ID AAU19837 standard; protein; 189 AA.
XX
AC AAU19837;
```

```
XX
DT 04-DEC-2001 (first entry)
XX
DE Human novel extracellular matrix protein, Seg ID No 487.
XX
KW Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV;
KW anti-neumatic; antithrombotic; antisclerotic; cardiac; vascular;
KW cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
KW antialzheimer; immune/autoimmune disease; HIV infection; anaemia;
KW human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;
KW cancer; hyperproliferative disorder; breast neoplasm; melanoma;
KW Sezary syndrome; Gaucher's disease; neurological diseases;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
KW cardiac arrest; tachycardia; angina; infection; corneal infections;
KW wound healing; immunogen; gene therapy; antisense; food additive.
XX
OS Homo sapiens.
XX
PN WO20015368-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001348.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0188874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226682P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
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PR	01-NOV-2000;	2000US-0249300P.	XX
PR	01-DEC-2000;	2000US-0250160P.	XX
PR	01-DEC-2000;	2000US-0250391P.	XX
PR	05-DEC-2000;	2000US-0251030P.	XX
PR	05-DEC-2000;	2000US-0251988P.	XX
PR	05-DEC-2000;	2000US-0251719P.	XX
PR	06-DEC-2000;	2000US-0251479P.	XX
PR	08-DEC-2000;	2000US-0251856P.	XX
PR	08-DEC-2000;	2000US-0251865P.	XX
PR	08-DEC-2000;	2000US-0251869P.	XX
PR	08-DEC-2000;	2000US-0251989P.	XX
PR	08-DEC-2000;	2000US-0251990P.	XX
PR	11-DEC-2000;	2000US-0254097P.	XX
PR	05-JAN-2001;	2001US-0259678P.	XX
PA	(HUMA-)	HUMAN GENOME SCI INC.	XX
PI	Rosen CA,	Baraash SC, Ruben SM;	XX
XX	WPI:	2001-465572/50.	XX
DR	N-P5DB:	AAS31408.	XX
PT	Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.		XX
XX	Claim 11; SEQ ID NO 487; 577pp; English.		XX
CC	The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease) cardio-/cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, support of cell culture of primary		CC
Query Match	16.1%;	Score 165;	DB 4; Length 189;
Best Local Similarity	28.8%;	Pred. No. 1.2e-08;	
Matches	36;	Conservative	24; Mismatches 53; Indels 12; Gaps 5
QY	69	CASCPs-CPDRMKYGNHCYFVSVEKQWNSLSERCLARDSHLYITTNQENSLLOVPLS	127
DB	68	CIKCEAPCEPDMLILGRCYCFSEBPPRMWNTGROYCHTHEVLAIVIOSQKELEFNFKEF-T	126
QY	128	EAFWIGIGLGN-NSGWRWEDGSPILNRSISNSFV-----QTGAIKNGKLGQASSCEVPLHG	182
DB	127	RRPPIGILRRVODEPHWVNGDPPD-----PDTITAGGEGCYFVPEPTRLVSTECMLTRPW	181
QY	183	VCKKV 187	
DB	182	VCSKM 186	
RESULT 11			
ID	ABBI7910	standard; protein; 189 AA.	
XX	ABBI7910	standard; protein; 189 AA.	

AC ABB17910;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polypeptide SEQ ID NO 6567.
XX
KW Human; nootropic; neuroprotective; cyostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischizoid; antianaemic; antithrombotic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
OS
XX Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001334.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229309P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234977P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235836P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239937P.
PR 13-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
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PR 20-OCT-2000; 2000US-0241786P.
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PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
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PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
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PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.

PR	02-OCT-2000	2000US-0236602P.
PR	02-OCT-2000	2000US-0237033P.
PR	02-OCT-2000	2000US-0237038P.
PR	02-OCT-2000	2000US-0237039P.
PR	02-OCT-2000	2000US-0237040P.
PR	13-OCT-2000	2000US-0239933P.
PR	13-OCT-2000	2000US-0239937P.
PR	20-OCT-2000	2000US-0240960P.
PR	20-OCT-2000	2000US-0241808P.
PR	20-OCT-2000	2000US-0241809P.
PR	20-OCT-2000	2000US-0241826P.
PR	01-NOV-2000	2000US-0244617P.
PR	01-NOV-2000	2000US-0244617P.
PR	08-NOV-2000	2000US-0246474P.
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PR	08-NOV-2000	2000US-0246613P.
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PR	17-NOV-2000	2000US-0249210P.
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PR	17-NOV-2000	2000US-0249213P.
PR	17-NOV-2000	2000US-0249215P.
PR	17-NOV-2000	2000US-0249215P.
PR	17-NOV-2000	2000US-0249216P.
PR	17-NOV-2000	2000US-0249218P.
PR	17-NOV-2000	2000US-0249218P.
PR	17-NOV-2000	2000US-0249244P.
PR	17-NOV-2000	2000US-0249245P.
PR	17-NOV-2000	2000US-0249264P.
PR	17-NOV-2000	2000US-0249265P.
PR	17-NOV-2000	2000US-0249287P.
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PR	05-DEC-2000	2000US-0251030P.
PR	05-DEC-2000	2000US-0251988P.
PR	05-DEC-2000	2000US-0256719P.
PR	06-DEC-2000	2000US-0251479P.
PR	08-DEC-2000	2000US-0251866P.
PR	08-DEC-2000	2000US-0251868P.
PR	08-DEC-2000	2000US-0251869P.
PR	08-DEC-2000	2000US-0251899P.
PR	11-DEC-2000	2000US-0251990P.
PR	05-JAN-2001	2000US-0259678P.
PR	17-JAN-2001	2000US-0264670.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM, Barash SC	
XX		
DR	WPI: 2003-743765/70.	
XX	N-P5DB; ADC10754.	

PT New isolated nucleic acids and polypeptides, useful for diagnosing,
 PT treating, and/or preventing disorders, such as cancer, infections,
 PT cardiovascular and inflammatory diseases.
 XX
 XX
 PS Claim 11; SEQ ID NO 487; 235pp; English.
 CC
 CC The invention relates to an isolated nucleic acid molecule (cdna)
 CC encoding a human extracellular matrix protein, representing one of 161
 CC novel genes. Also included are recombinant vectors, host cells
 CC (expressing the protein), the extracellular matrix proteins (including
 CC their fragments, epitopes and homologues), an isolated antibody that
 CC binds specifically to the protein, diagnosing a pathological condition or
 CC susceptibility to a pathological condition (comprising determining the
 CC presence or absence of a mutation in the nucleic acid and diagnosing a
 CC condition based on the presence or absence of the mutation), diagnosing a
 CC pathological condition or susceptibility to a pathological condition
 CC (comprising determining the presence or amount of expression of the
 CC protein in a biological sample and diagnosing a condition based on the
 CC presence or amount of expression of the protein), preventing, treating or
 CC ameliorating a medical condition by administering the nucleic acid or
 CC protein to a mammalian subject, identifying a binding partner to the
 CC protein, the gene corresponding to the cDNA sequence, and identifying an
 CC activity in a biological assay (comprising expressing the nucleic acid in
 CC a cell, isolating the supernatant, detecting an activity in a biological
 CC assay and identifying the protein in the supernatant having the
 CC activity). The nucleic acids and proteins display the following
 CC activities: Cytostatic, antibacterial, virucide, Neuroprotective,
 CC Gynaecological, Gastrointestinal-Gen, Cardiac, Cardiovascular-Gen,
 CC Nephrologic, Antiinflammatory, Muscular-Gen, Respiratory-Gen,

	Query Match Similarity	16.1%; Score 165; DB 7; Length 189;
	Best Local Similarity	28.8%; Pred.No. 1.2e-08;
	Matches	36; Conservative 24; Mismatches 53; Indels 12; Gaps 5
Dy	69 CASCPG-CPEDRMKYGNHCYPYSVEKDWNSSLEFCIARDSHLVTITNQEMSLQVFLS	127
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Dd	68 CIKCAAPCEBDWLTLYGRKCYPFSEBPRDWTGRQYCHTAEAVLAVIQSOKELFMFKF-T	126
	: : :	
Dy	128 EAFWCITGLRN-NSGMRWEDGSPLNFSRISNFV---QTGGAINNGHQAASCEVPPLHG	182
	: : :	
Dd	127 RREPPIGIRRVGDDEHFHWNGDPFD----PDFTIAGPGECVFVEPTRLVSTECIMTRPW	181
	: : :	
Dy	183 VCKKV 187	
	:	
Dd	182 VCCKM 186	
	:	
 RESULT 14 AAM78675		
ID	AAM78675 standard; protein; 188 AA.	
XX	AAM78675;	
AC		
DT	06-NOV-2001 (first entry)	
XX		
DE	Human protein SEQ ID NO 1337.	
XX		
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis;	
KM	tissue growth factor; immunomodulatory; cancer; leukaemia;	
KW	nervous system disorder; arthritis; inflammation.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200157190-A2.	
XX		
PD	09-AUG-2001.	
XX		
PF	05-FEB-2001; 2001WO-USO04098.	
XX		
PR	03-FEB-2000; 2000US-00496914.	
PR	27-APR-2000; 2000US-00560875.	
PR	20-JUN-2000; 2000US-00598075.	

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PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX N-PSDB; AAK51808.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 20; Page 3580; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAH80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication
XX
XX Sequence 188 AA;
XX
XX Query Match          15.5%; Score 159; DB 4; Length 188;
XX Best Local Similarity 26.5%; Pred. No. 5e-08;
XX Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;
XX
OY 41 ITLGLTAVLVSV-----LLYQWILCOGSN-----YSTC-----ASCPs----- 74
DB 6 IISGLIVVVLKVKVGMTLFLILYFPQIFNKNDGFTTTSYGVSOIFGSSSPSPNGFITTR 65
OY 75 -----CPDRMKYGNHCYFVSVEKDMNSLSEFCIARDSHLVTIDNOMSLLOVFLSEA 129
DB 66 SYGTVCPCDWEPYQARCFPLSTSESSWNSRDFCKGKSTLAIWTPPELKLQDITDAE 125
OY 130 FCWIGL---RNNSGRMEDGSPINFSRISNSFVOTCGAIN-KNGLQASSCEVPLHGYCK 185
DB 126 KYFGLIHYREKRWKRWINSVFN-GVNTNQNQNFNCATIGLTPTPDASCDISYRRICE 184
OY
OY 186 K 186
DB 185 K 185
XX
XX RESULT 15
XX ID AAU00671 standard; protein; 188 AA.
XX AC AAU00671;
XX
XX 07-SEP-2001 (first entry)
XX
XX Human INTERCEPT 289 form 1a polypeptide.
XX
XX Human; INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain;
XX skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;
XX bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;
XX anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease;
XX malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
XX attention deficit disorder; Crohn's disease; gastroenteritis; goitre;

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KW hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
KW muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 7..27
XX FT Domain /note= "Transmembrane domain"
XX FT Domain 28..188
XX FT Domain /note= "Extracellular domain"
XX
XX WO200129088-A1.
XX
XX 26-APR-2001.
XX
XX 23-JUN-2000; 2000WO-US017386.
XX
XX 19-OCT-1999; 99US-00420707.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Mackay CR, Myers PS, Kirst SJ, Fraser CC, Leiby KR;
XX WPI; 2001-308477/32.
XX N-PSDB; AAS00661.
XX
XX New isolated nucleic acid molecule for diagnosis, prevention, and therapy
XX of human and other animal disorder, or as modulating agent for regulating
XX cellular processes.
XX
XX Claim 8; Fig 2A-2B; 263pp; English.
XX
XX The sequence represents human INTERCEPT 289 form 1a polypeptide. This
XX protein and similar others exhibit the ability to affect growth,
XX proliferation, survival, differentiation, activity, morphology, or
XX movement/migration of, e.g. T cells and cells of the heart, liver,
XX pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph
XX node, peripheral blood leukocyte, bone marrow or thymus tissue. They can
XX be used as modulating agents for regulating cellular processes, thus, the
XX proteins and their associated nucleic acids can be used to prognosticate,
XX prevent, diagnose, or treat disorders associated with physiological
XX processes. These disorders include abnormal blood coagulation, asthma,
XX anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery
XX disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis,
XX meningitis, attention deficit disorder, Crohn's disease, gastroenteritis,
XX goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary
XX embolism and muscular dystrophy. Antibodies to disorders such as these
XX can be made by providing a polypeptide of the invention to an immuno-
XX competent vertebrate and harvesting blood or serum from the vertebrate
XX
XX Sequence 188 AA;
XX
XX Query Match          15.5%; Score 159; DB 4; Length 188;
XX Best Local Similarity 26.5%; Pred. No. 5e-08;
XX Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;
XX
OY 41 ITLGLTAVLVSV-----LLYQWILCOGSN-----YSTC-----ASCPs----- 74
DB 6 IISGLIVVVLKVKVGMTLFLILYFPQIFNKNDGFTTTSYGVSOIFGSSSPSPNGFITTR 65
OY 75 -----CPDRMKYGNHCYFVSVEKDMNSLSEFCIARDSHLVTIDNOMSLLOVFLSEA 129
DB 66 SYGTVCPCDWEPYQARCFPLSTSESSWNSRDFCKGKSTLAIWTPPELKLQDITDAE 125
OY 130 FCWIGL---RNNSGRMEDGSPINFSRISNSFVOTCGAIN-KNGLQASSCEVPLHGYCK 185
DB 126 KYFGLIHYREKRWKRWINSVFN-GVNTNQNQNFNCATIGLTPTPDASCDISYRRICE 184
OY
OY 186 K 186
DB 185 K 185

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Tue Jan 10 09:41:25 2006

us-09-811-367b-1.rag

Page 13

Search completed: January 9, 2006, 15:30:24
Job time : 90.977 secs

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/ APPLICANT: Hayden-Jedbetter, Martha S.
/ TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
/ FILE REFERENCE: 390069.401C1
/ CURRENT APPLICATION NUMBER: US/10/207,655
/ CURRENT FILING DATE: 2002-07-25
/ NUMBER OF SEQ ID NOS: 426
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO: 196
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-207-655-196

Query Match          98.4%; Score 1007; DB 4; Length 189;
Best Local Similarity 98.4%; Pred. No. 2.5e-92;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVITYSMLELPRTAQONDYGPQOKSSSKPSCGLVAITLGLITAVLSVLLYQWL 60
DB 1 MTDVITYSMLELPRTAQONDYGPQOKSSSKPSCGLVAITLGLITAVLSVLLYQWL 60
QY 61 COGSNYSTCASCPCSPDRMKYGNHCYFVSVEKQWNSLFECLARDSHLVTITNOEWS 120
DB 61 COGSNYSTCASCPCSPDRMKYGNHCYFVSVEKQWNSLFECLARDSHLVTITNOEWS 120
QY 121 LLQVFLSEAFQWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180
DB 121 LLQVFLSEAFQWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HGVCCKVRL 189

RESULT 3
US-10-756-149-5210
/ Sequence 5210, Application US/10756149
/ Publication No. US20050181375A1
/ GENERAL INFORMATION:
/ APPLICANT: Aziz, Natsaba
/ APPLICANT: Zlocznik, Albert
/ TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
/ FILE REFERENCE: file
/ CURRENT APPLICATION NUMBER: US/10/756,149
/ CURRENT FILING DATE: 2004-01-12
/ NUMBER OF SEQ ID NOS: 5818
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO: 5210
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-756-149-5210

Query Match          98.4%; Score 1007; DB 5; Length 189;
Best Local Similarity 98.4%; Pred. No. 2.5e-92;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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RESULT 4
US-09-811-367B-3
/ Sequence 3, Application US/09811367B
/ Patent No. US20020155110A1
/ GENERAL INFORMATION:
/ APPLICANT: GEMINI SCIENCE, INC.
/ APPLICANT: Takahashi, No. US20020155110A1uak1
/ APPLICANT: Mikayama, Toshifumi
/ TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
/ FILE REFERENCE: 021286/0278719
/ CURRENT APPLICATION NUMBER: US/09/811,367B
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 60/190,716
/ PRIOR FILING DATE: 2000-03-17
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO: 3
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-811-367B-3
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Query Match          53.6%; Score 548.5; DB 3; Length 188;
Best Local Similarity 55.6%; Pred. No. 1.7e-46;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDVITYSMLELPRTAQONDYGPQOKSSSKPSCGLVAITLGLITAVLSVLLYQWL 60
DB 1 MADSSIVSTLELPAPQVQDSRWELKAVLRPHLSRPAMVALGILLTILMSLWYORL 60
QY 61 COGSNYSTCASCPCSPDRMKYGNHCYFVSVEKQWNSLFECLARDSHLVTITNOEWS 120
DB 61 COGSNYSTCASCPCSPDRMKYGNHCYFVSVEKQWNSLFECLARDSHLVTITNOEWS 120
QY 121 LLQVFLSEAFQWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180
DB 121 LLQVFLSEAFQWIGLRNNSGMRWEDGSPINFGRISNSFVQTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKV 187
DB 180 QWICKV 186
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RESULT 5
US-09-811-367B-5
/ Sequence 5, Application US/09811367B
/ Patent No. US20020155110A1
/ GENERAL INFORMATION:
/ APPLICANT: GEMINI SCIENCE, INC.
/ APPLICANT: Takahashi, No. US20020155110A1uak1
/ APPLICANT: Mikayama, Toshifumi
/ TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
/ FILE REFERENCE: 021286/0278719
/ CURRENT APPLICATION NUMBER: US/09/811,367B
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 60/190,716
/ PRIOR FILING DATE: 2000-03-17
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO: 5
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-09-811-367B-5
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Query Match          51.4%; Score 525.5; DB 3; Length 188;
Best Local Similarity 53.5%; Pred. No. 3.4e-44;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
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QY 1 TTDSIVSYMLETPTNTOANDYGPQOKSSSKRSCGLVAITGLTAVLSTLVKOWIL 60
Db 1 MADSNIYSTLELPALPRVODDSRMWKVAVIHRPCVSLVMAVAGLTLVILMSLLVQRTL 60
QY 61 CCGSNYSTCASCPSCPDRMMKYGNHCYFYSVEBKDNSSLEFCLARDSHLVTITDQEMS 120
Db 61 CCGSGAGFMCSQCSRCPCNLMMRWBRGSHCYFYSMEKRDWNSSILKFCADKSHLLTTPPDQGVN 120
QY 121 LLOVLVLSFAFCVIGILRNNSGRWRWEDSPLNFSKILSSNSPVQTCGALINKKGLQASSCEVPL 180
Db 121 LFOEYVAGDFYVIGILRIDIDGWRWEDGPAISLS-ILSSNVVQCKGCTIHRCGLRASSCEVAL 179
QY 181 HGVCCKV 187
Db 180 QMICEKV 186

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RESULT 6
US-09-764-870-487
; Sequence 487, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT1214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 487
; LENGTH: 189
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-764-870-487

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Query Match	16.1%;	Score 165;	DB 3;	Length 189;
Best Local Similarity	28.8%;	Pred. No. 3.6e-08;		
Matches	36;	Conservative	24;	Mismatches 53;
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				Gaps 5;

[illegible]

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RESULT 7
US-10-125-540-487
; Sequence 487, Application US/10125540
; Publication No. US20030059875A1
GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P1214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; PRIORITY FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ. ID NO 487
; LENGTH: 189
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-125-540-487

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Query Match 16.1%; Score 165; DB 4; Length 189;

[illegible]

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RESULT 8
US-09-759-130B-83
/ Sequence 83, Application US/09759130B
/ Publication No. US20030022279A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: McCarthy, Sean A
/ APPLICANT: Fraser, Christopher C
/ APPLICANT: Sharp, John D
/ APPLICANT: Barnes, Thomas S
/ APPLICANT: Kirst, Susan J
/ APPLICANT: Mackay, Charles R
/ APPLICANT: Myers, Paul S
/ APPLICANT: Leiby, Kevin R
/ APPLICANT: Wrighton, Nicolas
/ APPLICANT: Goodheart, Andrew
/ APPLICANT: Holtzman, Douglas A
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
/ TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
/ FILE REFERENCE: MP100-5350NIM
/ CURRENT APPLICATION NUMBER: US/09/759,130B
/ CURRENT FILING DATE: 2002-09-16
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 83
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-759-130B-83

```

Query Match 15.5%; Score 159; DB 3; Length 186;
Best Local Similarity 26.5%; Pred. No. 1.4e-07;
Matches 48; Conservative 23; Mismatches 74; Gaps 7;

41 ITGLTAVLSV-----LYQMLCGSN-----YSTC-----ASCRS-----74

Db 6 IISGLIVVAKVGMFLFLIYFQIQINKNNDGFTTTRSGTVSQIFSSSSPSPNGFITTR 65

Qy 75 -----CPDRMKYGNHCYFYSVEKDMNSLFCICARDSHLLVITDQEMSLQVFLSEA 129

Db 66 SYGVGCPKDEYFQARCFPLSTSESSMNSRDFCGKSGTALIVTPEKLFQDIDTDAE 125

Qy 130 FCMIGL---RNSGKRWEDGSPINFRISNSFVOTCGAIN-KAGLQASCEVPLHGVCK 185

Db 126 KYFGLIYHREKRWKRWINNVSFVN-GNVTNQNQNFCAITGLTFTDAASCDISYRRICE 184

Qy 186 K 186

Db 185 K 185

RESULT 9

```

Sequence 83, Application US/10741790
Publication No. US20040121396A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirts, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Meyers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodheartl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE,
FILE REFERENCE: MP100-530MNM
CURRENT APPLICATION NUMBER: US/10/741,790
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 83
LENGTH: 188
TYPE: PRT
ORGANISM: Homo sapiens
US-10-741-790-83

```

Query Match	15.5%	Score 159;	DB 4;	Length 188;
Best Local Similarly	26.5%	Pred. NO.1.4e-07;		
Matches 48;	Conservative 23;	Mismatches 74;	Indels 36;	Gaps 7;

```

Oy      41 ITLGLTAVLLSV-----LLYQMLLCQGSN-----VSTC-----ASCP----- 74
      ||: || ||| : || ||| : |||
Db      6 IISGLIVVLKVVGMTELLYFQIFNKSNDGFTTTRSYGVTSQITGSSSSSPNGFTTR 65

```

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QY 75 -----CPBRMKYGMHCYFSEVEEDMNSLFCUARDSHLVTITNOEMLLOVFLSEA 1239
Db 66 SYGTVCPEKDMEFYQARCEFLSTSEBSWMSRPFCKGKGYLLAVNTPETKFLQDITDAE 1255
QY 130 FCMIGL-----RNNSGMRWEDGSPINFSRISNSFVOTCGALIN-KNGQASSCVEPLHGVC 1855
Db 126 KYFIDLIYHREKRWIRWINSVFN-GVNTNQNQNFNCATIGLTPTDAASCDISYRICE 1844
QY 186 K 186
Db 185 K 185

```

RESULT 10

```

/ Sequence 69, Application US/10/287436A
/ Publication No. US20050202421A1
/
/ GENERAL INFORMATION:
/
/ APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
/ TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
/ TITLE OF INVENTION: RHEDUMATOID ARTHRITIS
/ FILE REFERENCE: 10872.514696
/ CURRENT APPLICATION NUMBER: US/10/287,436A
/ CURRENT FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: US 60/336,220
/ PRIOR FILING DATE: 2001-10-31
/ NUMBER OF SEQ. ID NOS: 146
/ SOFTWARE: PatsSeq for Windows Version 4.0
/ SEQ ID NO 69
/
/ LENGTH: 188
/
/ TYPE: PRT
/
/ ORGANISM: Homo sapiens
/ US-10-287-436A-69

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Query Match	15.5%;	Score 159;	DB 5;	Length 188;
Best Local Similarity	26.5%;	Pred. No. 1.4e-07;		
Matches	48;	Conservative	23;	Mismatches 74;
			Indels	36;
			Gaps	7

QY 41 ITLGLHTLVLSV-----LIYOMILCOGSN-----YSTC-----ASCPs----- 74
 Db 6 IISGLIIVVLKRVGMLTFLLEFPQIFNKSNDFITTRSYGIVSQIFGSSSPENGFIITR 65
 QY 75 -----CPDRMMKYGNHCYVPSVEEKDMSSLEFCLARDSHLLVITDNOGMSLLQVPLSEA 129
 Db 66 SYGYTCPCDMETVQARCFPLSTSESSMNSRPFCKGKSLTIAVNPBKTKFLQDITDAE 125
 QY 130 FCMWGL-----RNSGNRMEDGSEPLNFSRISSNSFVOTCGAIN-KNGLQASSCEVPLHGVC 185
 Db 126 KYFISLIYHREKRWIRWINSVFN-GVNTQNGQNFNCATIGLTKTPDAASCDISYRICE 184
 QY 186 K 186
 Db 185 K 185

RESULT 11

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US-10-287-436A-1251
; Sequence 1251, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1251
;
; LENGTH: 188

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/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-436A-1251

Query Match      15.5%; Score 159; DB 5; Length 188;
Best Local Similarity 26.5%; Pred. No. 1,4e-07;
Matches 48; Conservative 23; Mismatches 74; Indels 36; Gaps 7;

QY 41 ITLGLTAVLTSV-----LLYQWILCGSN-----YSTC-----ASCPS-----74
DB 6 ITSGILVVLKVGMTLFLFYFQIIPKNSDGETTRTSYGTYSQIRGSSSPSPNGFITTR 65
QY 75 -----CPDRMKXGNHCYFVSVEKDNSSLEFCLARDSHLVITDQEMSLIQVFLSEA 129
DB 66 SYGTVCPEKMEFYQARCFILSTSESSWNESEKDFCKGKSTLAIWNPETKLFQDITDAE 125
QY 130 FCHIGL---RNSGMRWEDGSPINFRISNSFVOTCGAI-NKNGQASSCEVPLHGVCK 185
DB 126 KYFPIGLIYHREKRWKRWINSVFN-GNVTNQNQNFNCATIGLTXTFDASCDISYRICE 184
QY 186 K 186
DB 185 K 185

RESULT 12
US-11-097-143-5490
/ Sequence 5490, Application US/11097143
/ Publication No. US20050208558A1
/ GENERAL INFORMATION:
/ APPLICANT: Venter, J. Craig
/ APPLICANT: et al.
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/11/097,143
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: 60/157,832
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/160,191
/ PRIOR FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: 60/161,932
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5490
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-11-097-143-5490

Query Match      10.1%; Score 103.5; DB 6; Length 188;
Best Local Similarity 21.0%; Pred. No. 0.051;
Matches 39; Conservative 26; Mismatches 66; Indels 55; Gaps 9;

QY 49 VLSVLLYQWILC-----QGSNYSYTCASCPSC-----PDRW-----MKYGNHCYF 89
DB 5 LLSVILSLQGLCLLDRTMATPPKPGPVADCPNVCDSQYTPNKMTPMLPKLGEKRYYL 64
QY 90 SVEEK-DWNSLEFCLARDSHLVITDQEMSLIQVFLSEAFCHIGLRNNSGW-----141
DB 65 GIPFKAMFKATQYCRVYHMLASISQGEENDRLKHIRD---FGLGHEHFWISGTDLA 120
```

```
QY 142 -----RWEDGSPINFRISNSFVOTCGAI-NKNG-----LQASSCEVP 179
DB 121 DEGNFEMMATGRPIFTYNNAGEPNNFR--YENGEENCLIELMNDGKGLKWNDSFCSPE 178
QY 180 LHGVCK 185
DB 179 TYFVCE 184

RESULT 13
US-10-114-893-48
/ Sequence 48, Application US/10114893
/ Publication No. US20020193567A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: Treacy, Maurice
/ APPLICANT: McCoy, John M.
/ APPLICANT: Lavallee, Edward R.
/ APPLICANT: Collins-Racie, Lisa A.
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Weiberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Bowman, Michael R.
/ APPLICANT: Spaulding, Vikki
/ APPLICANT: Carlin-Duckett, McKeough
/ APPLICANT: Kelleher, Kerry S.
/ APPLICANT: Genetics Institute, Inc.
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
/ FILE REFERENCE: GI 6000-10A
/ CURRENT APPLICATION NUMBER: US/10/114,893
/ CURRENT FILING DATE: 2002-04-02
/ EARLIER APPLICATION NUMBER: 09/413,232
/ NUMBER OF SEQ ID NOS: 321
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 48
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-114-893-48

Query Match      9.8%; Score 100.5; DB 4; Length 189;
Best Local Similarity 37.3%; Pred. No. 0.1;
Matches 19; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 70 ASCPS-CPDRMKXGNHCYFVSVEKDNSSLEFCLARDSHLVITDQEM 119
DB 138 ANCSAPCPQDMWHGENCYLFSGSGFNWESQEKCLSLDKLKLKINSTADL 188

RESULT 14
US-10-369-493-5642
/ Sequence 5642, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 5642
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-369-493-5642
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Query Match 9.0%; Score 92.5; DB 4; Length 188;
Best Local Similarity 31.4%; Pred. No. 64;
Matches 27; Conservative 10; Mismatches 32; Indels 17; Gaps 4;

QY 79 WMKYGNHCYPSVEEKDNWNSLEFCLARDSHLVT---TDNQMSILOVFLSEA----- 129
DB 54 WFSYTNFCYKSPARAFNDANACRSEGSFLASIHSLTENQFL---VQLSAGNRVNS 109
QY 130 ---FCWIGL-RNNSGWRWEDGSPLNPF 151
DB 110 KTNVWIGLIFENREMSWTGSSVNY 135

RESULT 15

US-11-097-143-3261
; Sequence 3261, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3261
; LENGTH: 188
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-3261

Query Match 7.1%; Score 72.5; DB 6; Length 188;
Best Local Similarity 25.2%; Pred. No. 64;
Matches 31; Conservative 22; Mismatches 55; Indels 15; Gaps 6;

QY 45 LTTAVLLSVLYQWILCOGSNTST--CASCPCPCDR--WMKYGNHCYPSVEEK-DWNS 99
DB 10 ILTSVIGIPSLALPVDVNIPTNRTBYNGIPSEIDTTPVRIGDNYVTEPMNKXNMFQA 69
QY 100 LEFCLARDSHLVITDQMSLL-----QVFLSEAFWIG--LRNNSGWRW-EDGSP 149
DB 70 AGACRMNMNHLASIEDKPEMEALIKYMKAKGFKNNDYFWISGNDLGTGEGAFYWMGNGRPM 129
QY 150 NFS 152
DB 130 TYA 132

Search completed: January 9, 2006, 15:55:58
Job time : 73.9239 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:36:43 ; Search time 10.7044 Seconds
(without alignments)
149.966 Million cell updates/sec

Title: US-09-811-367b-1
Perfect score: 1023
Sequence: 1 MTDSVYISMLELPRTAQAQN.....GLQASSCEVPLHGCKKRVRL 189

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 61141 seqs, 8493638 residues
Total number of hits satisfying chosen parameters: 97

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA_New.*
1: /cgn2_6/pcodaca/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/pcodaca/2/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/pcodaca/2/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/pcodaca/2/pubppaa/PCR_NEW_PUB.pep.*
5: /cgn2_6/pcodaca/2/pubppaa/US05_NEW_PUB.pep.*
6: /cgn2_6/pcodaca/2/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/pcodaca/2/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/pcodaca/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	100.0	189	6	US-10-055-877-209
2	1007	98.4	189	6	US-10-055-877-207
3	548.5	53.6	188	6	US-10-055-877-205
4	525.5	51.4	188	6	US-10-055-877-206
5	47	4.6	189	7	US-11-147-492-30
6	44	4.3	189	6	US-10-821-234-1432
7	44	4.3	189	6	US-10-878-556A-193
8	42.5	4.2	188	6	US-10-980-388-90
9	41.5	4.1	189	7	US-11-147-492-10
10	41.5	4.1	189	7	US-11-147-492-20
11	41	4.0	189	7	US-11-137-465-60
12	40.5	4.0	189	7	US-11-147-492-28
13	38.5	3.8	189	7	US-11-147-492-24
14	38	3.7	188	6	US-10-467-657-2750
15	38	3.7	189	6	US-10-995-561-806
16	36.5	3.6	189	7	US-11-147-492-16
17	35.5	3.5	188	6	US-10-945-853-1
18	35.5	3.5	189	6	US-10-467-657-6250
19	35	3.4	189	6	US-10-821-234-1421
20	35	3.4	189	7	US-11-205-109-33
21	34.5	3.4	188	6	US-10-884-730-88
22	34.5	3.4	188	6	US-10-945-853-2
23	33	3.2	188	7	US-11-064-774A-117
24	33	3.2	189	7	US-10-131-826A-240
25	33	3.2	189	6	US-10-467-657-3184

26	33	3.2	189	7	US-11-147-492-26	Sequence 26, Appl
27	32.5	3.2	188	6	US-10-980-388-101	Sequence 101, App
28	32.5	3.2	189	7	US-11-147-492-12	Sequence 12, Appl
29	32	3.1	188	7	US-11-055-822-152	Sequence 192, App
30	31.5	3.1	188	6	US-10-467-657-4044	Sequence 4044, Ap
31	31	3.0	189	6	US-10-467-657-920	Sequence 920, App
32	31	3.0	188	7	US-11-000-463-866	Sequence 866, App
33	31	3.0	188	7	US-11-000-463-867	Sequence 867, App
34	31	3.0	189	6	US-10-467-657-4692	Sequence 4692, Ap
35	31	3.0	189	7	US-11-071-262-1	Sequence 1, Appli
36	31	3.0	189	7	US-11-147-492-6	Sequence 6, Appli
37	31	3.0	189	7	US-11-147-492-22	Sequence 22, Appl
38	30.5	3.0	188	6	US-10-842-206-40	Sequence 40, Appl
39	30.5	3.0	188	6	US-10-980-459-32	Sequence 32, Appl
40	30.5	3.0	188	7	US-11-147-492-8	Sequence 8, Appli
41	30	2.9	188	6	US-10-131-826A-2	Sequence 2, Appli
42	30	2.9	188	6	US-10-793-626-152	Sequence 152, App
43	30	2.9	188	6	US-10-821-234-1316	Sequence 1316, Ap
44	30	2.9	188	7	US-11-054-515-3235	Sequence 3235, Ap
45	30	2.9	188	7	US-11-194-246-292	Sequence 292, App

ALIGNMENTS

RESULT 1
US-10-055-877-209
; Sequence 209, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padisaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Veltzar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Wezes, Peter
; APPLICANT: Patuturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Bisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkete, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OR INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,992
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25

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/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ PRIOR FILING DATE: 2001-03-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 209
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-055-877-209

Query Match          100.0%; Score 1023; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 5.3e-100;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVYISMLELPTATQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60
DB 1 MTDVYISMLELPTATQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60
QY 61 CQGSNYSITCASCPSPCDPRMKNKGNHCYFVSVEKDMNSSLFECCLARDSHLLVITDQEMS 120
DB 61 CQGSNYSITCASCPSPCDPRMKNKGNHCYFVSVEKDMNSSLFECCLARDSHLLVITDQEMS 120
QY 121 LLQVFLSEAFQWIGLRNNSGWRMEDGSPINFRISSNSFVOTCGAINKNGLOASSCEVPL 180
DB 121 LLQVFLSEAFQWIGLRNNSGWRMEDGSPINFRISSNSFVOTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HGVCCKVRL 189

RESULT 2
US-10-055-877-207
/ Sequence 207, Application US/10055877
/ Publication No. US20050288241A1
/ GENERAL INFORMATION:
/ APPLICANT: Decristofaro, Marc
/ APPLICANT: Padigarlu, Muralidhara
/ APPLICANT: Miller, Charles
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Zhong, Mei
/ APPLICANT: Anderson, David
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Rattelli, Luca
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Zernhuusen, Bryan
/ APPLICANT: Andrew, David
/ APPLICANT: Mezes, Peter
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Eising, Andrew
/ APPLICANT: Wolenc, Adam
/ APPLICANT: Baumgartner, Jason
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Vernet, Corine
/ APPLICANT: Taupier Jr., Raymond
/ APPLICANT: Pena, Carol
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Li, Li
/ APPLICANT: Casman, Stacie
```

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/ APPLICANT: Boldog, Ference
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
/ FILE REFERENCE: 21402-251
/ CURRENT APPLICATION NUMBER: US/10/055,877
/ PRIOR FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,598
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/263,799
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/264,117
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,139
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 207
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-055-877-207

Query Match          98.4%; Score 1007; DB 6; Length 189;
Best Local Similarity 98.4%; Pred. No. 2.5e-98;
Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDVYISMLELPTATQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60
DB 1 MTDVYISMLELPTATQANDYGPQOKSSSKPSCSCVAITLGLITVLLSVLLYQWIL 60
QY 61 CQGSNYSITCASCPSPCDPRMKNKGNHCYFVSVEKDMNSSLFECCLARDSHLLVITDQEMS 120
DB 61 CQGSNYSITCASCPSPCDPRMKNKGNHCYFVSVEKDMNSSLFECCLARDSHLLVITDQEMS 120
QY 121 LLQVFLSEAFQWIGLRNNSGWRMEDGSPINFRISSNSFVOTCGAINKNGLOASSCEVPL 180
DB 121 LLQVFLSEAFQWIGLRNNSGWRMEDGSPINFRISSNSFVOTCGAINKNGLOASSCEVPL 180
QY 181 HGVCCKVRL 189
DB 181 HGVCCKVRL 189

RESULT 3
US-10-055-877-205
/ Sequence 205, Application US/10055877
/ Publication No. US20050288241A1
/ GENERAL INFORMATION:
/ APPLICANT: Decristofaro, Marc
/ APPLICANT: Padigarlu, Muralidhara
/ APPLICANT: Miller, Charles
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Zhong, Mei
/ APPLICANT: Anderson, David
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Rattelli, Luca
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Zernhuusen, Bryan
```

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/ APPLICANT: Andrew, David
/ APPLICANT: Mezes, Peter
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Eileen, Andrew
/ APPLICANT: Wolenc, Adam
/ APPLICANT: Baumgartner, Jason
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Vernet, Corine
/ APPLICANT: Taupier Jr., Raymond
/ APPLICANT: Pena, Carol
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Li, Li
/ APPLICANT: Casman, Stacie
/ APPLICANT: Boldog, Ferenc
/ APPLICANT:
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
/ FILE REFERENCE: 21402-251
/ CURRENT APPLICATION NUMBER: US/10/055,877
/ PRIOR FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,598
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/263,799
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/264,117
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,139
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ PRIOR FILING DATE: 2001-03-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 205
/ LENGTH: 188
/ TYPE: PRF
/ ORGANISM: Mus musculus
/ US-10-055-877-205

Query Match      53.6%; Score 548.5; DB 6; Length 188;
Best Local Similarity 55.6%; Pred. No. 1.8e-50;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY      1 MTDVSIYSMLLPATQAQNDYGPQOKSSSKSCGLVATTGLTFAVLVSLTYOMIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MADNSIYSTLELPAPAVQDESRLKAVLHPRHLSFPAWVALGLTVIILMSLTYORTL 60

QY      61 CQGSNVTCTASCSPBCPRRMKYGNGHCYFVSVEKDNMSLJFCLARDSHLLVTIDNEMS 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 CCGSKDSTCTCHPCPCPLMTWTNGSHCYFVSMEKDNMSLJFCLARDSHLLTPFDNCGVK 120

QY      121 LLYVFLSEAFCMWGLRNNSGWRWEDGSPFNFSRISNSPVOTCGAINKNGLOASSCEVPL 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 LFGVYLDQDFYWIIGLRINIDGWRWEGPALSL-RLTITSLIGRCALHNRNGLOASSCEVAL 179

QY      181 HGVCCKV 187
      :||||
Db      180 QWICKV 186

RESULT 4
US-10-055-877-206
/ Sequence 206, Application US/10055877
```

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/ Publication No. US20050288241A1
/ GENERAL INFORMATION:
/ APPLICANT: Decristofaro, Marc
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Miller, Charles
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Zhong, Mei
/ APPLICANT: Anderson, David
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Ratelli, Luca
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Zernhusen, Bryan
/ APPLICANT: Andrew, David
/ APPLICANT: Mezes, Peter
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Eileen, Andrew
/ APPLICANT: Wolenc, Adam
/ APPLICANT: Baumgartner, Jason
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Vernet, Corine
/ APPLICANT: Taupier Jr., Raymond
/ APPLICANT: Pena, Carol
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Li, Li
/ APPLICANT: Casman, Stacie
/ APPLICANT: Boldog, Ferenc
/ APPLICANT:
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
/ FILE REFERENCE: 21402-251
/ CURRENT APPLICATION NUMBER: US/10/055,877
/ PRIOR FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,598
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/263,799
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/264,117
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,139
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 206
/ LENGTH: 188
/ TYPE: PRF
/ ORGANISM: Rattus norvegicus
/ US-10-055-877-206

Query Match      51.4%; Score 525.5; DB 6; Length 188;
Best Local Similarity 53.5%; Pred. No. 4.6e-48;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY      1 MTDVSIYSMLLPATQAQNDYGPQOKSSSKSCGLVATTGLTFAVLVSLTYOMIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MADNSIYSTLELPAPAVQDESRLKAVLHPRHLSFPAWVALGLTVIILMSLTYORTL 60

QY      61 CQGSNVTCTASCSPBCPRRMKYGNGHCYFVSVEKDNMSLJFCLARDSHLLVTIDNEMS 120
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1432

Query Match      4.3%; Score 44; DB 6; Length 189;
Beet Local Similarity 24.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 16; Mismatches 41; Indels 30; Gaps 5;

QY 7 YSMLELPATQAONDYGPQOKSSSS-----KPSCSCLVAITGLTAVLLSVLYQW 58
DB 67 YDVVVL P-----GNNLGAQNI SESAAVKEILKEQENRKGLIAICAGPALLAHRIGF-- 119

QY 59 ILCOGSNSTGSCAPCDPRMVKYGNHCYFSVEEKD-----NSSLFCL 105
DB 120 ----GSKVTT---HPLAKDKMNGGHYTYSENRYEKDGLILTSRGPSTSFEPALA 167

RESULT 7
US-10-878-556A-193
; Sequence 193, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: US 60/579,024
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1.1
; SEQ ID NO 193
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: human9p/chr1-014805
; DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-193

Query Match      4.3%; Score 44; DB 6; Length 189;
Beet Local Similarity 24.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 16; Mismatches 41; Indels 30; Gaps 5;

QY 7 YSMLELPATQAONDYGPQOKSSSS-----KPSCSCLVAITGLTAVLLSVLYQW 58
DB 67 YDVVVL P-----GNNLGAQNI SESAAVKEILKEQENRKGLIAICAGPALLAHRIGF-- 119

QY 59 ILCOGSNSTGSCAPCDPRMVKYGNHCYFSVEEKD-----NSSLFCL 105
DB 120 ----GSKVTT---HPLAKDKMNGGHYTYSENRYEKDGLILTSRGPSTSFEPALA 167

RESULT 8
US-10-980-388-90
; Sequence 90, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaye, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325, US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304

US-11-147-492-30
; Sequence 30, Application US/11147492
; Publication No. US20050276785A1
; GENERAL INFORMATION:
; APPLICANT: Kapp, Joachim-Freidrich
; APPLICANT: Kuehl, Uwe
; APPLICANT: Groetzsch, Georg
; APPLICANT: Schultheis, Heinz-Peter
; APPLICANT: Sowade, Olaf
; APPLICANT: Stuerzebecher, Claus-Steffen
; TITLE OF INVENTION: Treatment of Cardiomypathy and Endothelial Dysfunction
; FILE REFERENCE: 53223
; CURRENT APPLICATION NUMBER: US/11/147,492
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/579,024
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 189
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-147-492-30

Query Match      4.6%; Score 47; DB 7; Length 189;
Beet Local Similarity 24.2%; Pred. No. 4.3e+02;
Matches 40; Conservative 20; Mismatches 57; Indels 48; Gaps 10;

QY 39 VAITGLTAVLLSVLYQWILCOGSNSTGSCAP-----SC-PDRM 80
DB 1 MALSSLLMAVL--VLSYKICSLGCDLPQTHSLGNRRALILAQGRISPSCLKDR-- 56

QY 81 KGNHCYFSVEEKDMSSELCLARDSHLVITTNQESLLOVLSSEFCWIGLRNSG 140
DB 57 ----HDFGPQEEFGN--QFOKA-----QALSVLHEMIQOTFNLFTKDS 98

QY 141 WRMEDGSPINFRISNSF--VOTCGAINKGLQASSCEVPLHGV 183
DB 99 -TWEGSLEKFEFTLNQQLNDMEAC-VIOEGVE---ETPLMNV 137

RESULT 6
US-10-821-234-1432
; Sequence 1432, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1432
; LENGTH: 189

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```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1432

Query Match      4.3%; Score 44; DB 6; Length 189;
Beet Local Similarity 24.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 16; Mismatches 41; Indels 30; Gaps 5;

QY 7 YSMLELPATQAONDYGPQOKSSSS-----KPSCSCLVAITGLTAVLLSVLYQW 58
DB 67 YDVVVL P-----GNNLGAQNI SESAAVKEILKEQENRKGLIAICAGPALLAHRIGF-- 119

QY 59 ILCOGSNSTGSCAPCDPRMVKYGNHCYFSVEEKD-----NSSLFCL 105
DB 120 ----GSKVTT---HPLAKDKMNGGHYTYSENRYEKDGLILTSRGPSTSFEPALA 167

RESULT 7
US-10-878-556A-193
; Sequence 193, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; PRIOR APPLICATION NUMBER: US 60/579,024
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1.1
; SEQ ID NO 193
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: human9p/chr1-014805
; DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-193

Query Match      4.3%; Score 44; DB 6; Length 189;
Beet Local Similarity 24.3%; Pred. No. 8.7e+02;
Matches 28; Conservative 16; Mismatches 41; Indels 30; Gaps 5;

QY 7 YSMLELPATQAONDYGPQOKSSSS-----KPSCSCLVAITGLTAVLLSVLYQW 58
DB 67 YDVVVL P-----GNNLGAQNI SESAAVKEILKEQENRKGLIAICAGPALLAHRIGF-- 119

QY 59 ILCOGSNSTGSCAPCDPRMVKYGNHCYFSVEEKD-----NSSLFCL 105
DB 120 ----GSKVTT---HPLAKDKMNGGHYTYSENRYEKDGLILTSRGPSTSFEPALA 167

RESULT 8
US-10-980-388-90
; Sequence 90, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaye, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325, US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304

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/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,303
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,397
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/184,247
/ PRIOR FILING DATE: 2000-02-23
/ PRIOR APPLICATION NUMBER: 60/188,880
/ PRIOR FILING DATE: 2000-03-13
/ PRIOR APPLICATION NUMBER: 60/217,369
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/217,370
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/218,492
/ PRIOR FILING DATE: 2000-07-20
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 184
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 90
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-980-388-90

Query Match
Best Local Similarity 21.8%; Score 42.5; DB 6; Length 188;
Matches 24; Conservative 15; Mismatches 36; Indels 35; Gaps 6;

QY 64 SNVSTCASC-----SCPRMKNYK-----NHCVFVSVEEKDNNSSLEFCLARDSHLVTVDNQ 117
DB 26 SQSCCTQTLPLNCLDLYFGKTKTNLYF-----TTTFSLHESYSLEI---Q 72
QY 118 EMSLQVFLSEAFPCWIGLRNNSGWRWEDGSPLNFSRISNSFYVOTCGAIN 167
DB 73 LFPKLTKESSPF-----SGEP--FPVLEDSFQRCQGNW 106

RESULT 9
US-11-147-492-10
/ Sequence 10, Application US/11147492
/ Publication No. US20050276785A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapp, Joachim-Freidrich
/ APPLICANT: Kuehl, Uwe
/ APPLICANT: Groetzbach, Georg
/ APPLICANT: Schulteises, Heinz-Peter
/ APPLICANT: Sowade, Olaf
/ APPLICANT: Stuerzebecher, Claus-Steffen
/ TITLE OF INVENTION: Treatment of Cardiomypathy and Endothelial Dysfunction
/ FILE REFERENCE: 53223
/ CURRENT APPLICATION NUMBER: US/11/147,492
/ PRIOR FILING DATE: 2005-06-07
/ PRIOR APPLICATION NUMBER: US 60/579,024
/ PRIOR FILING DATE: 2004-06-04
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 10
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-147-492-10

Query Match
Best Local Similarity 4.1%; Score 41.5; DB 7; Length 189;
Matches 31; Conservative 14; Mismatches 39; Indels 37; Gaps 6;
```

```
QY 130 F 130
DB 113 Y 113

RESULT 10
US-11-147-492-20
/ Sequence 20, Application US/11147492
/ Publication No. US20050276785A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapp, Joachim-Freidrich
/ APPLICANT: Kuehl, Uwe
/ APPLICANT: Groetzbach, Georg
/ APPLICANT: Schulteises, Heinz-Peter
/ APPLICANT: Sowade, Olaf
/ APPLICANT: Stuerzebecher, Claus-Steffen
/ TITLE OF INVENTION: Treatment of Cardiomypathy and Endothelial Dysfunction
/ FILE REFERENCE: 53223
/ CURRENT APPLICATION NUMBER: US/11/147,492
/ PRIOR FILING DATE: 2005-06-07
/ PRIOR APPLICATION NUMBER: US 60/579,024
/ PRIOR FILING DATE: 2004-06-04
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 20
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-147-492-20

Query Match
Best Local Similarity 4.1%; Score 41.5; DB 7; Length 189;
Matches 31; Conservative 13; Mismatches 40; Indels 37; Gaps 6;

QY 39 VAITGLTAVLTVLTVLQWILCOGNSYSTCASC-----SC-PDRWM 80
DB 1 MALSPSLMANVL--VLSYKSLGCDLPQTHSLGNRRALLILQMGRIHSFSCIKOR-- 56
QY 81 KYGNHCYFVSVEEKDNN-----SLEFCLARDSHLVTVDNQ---EMSLQVFLSEA 129
DB 57 ----HDFRIPQEEFDGNOFQKAQALSVLHEMIQOTFNLFSTEDSSAMEOSLLEKFSTEL 112
QY 130 F 130
DB 113 Y 113

RESULT 11
US-11-137-465-60
/ Sequence 60, Application US/11137465
/ Publication No. US2005025558A1
/ GENERAL INFORMATION:
/ APPLICANT: Agarwal, Pankaj
/ APPLICANT: Murdoch, Paul R.
/ APPLICANT: Rizvi, Safia, K.
/ APPLICANT: Smith, Randall, F.
/ APPLICANT: Xiang, Zhaoying
/ APPLICANT: Kadnick, Karen
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50018
/ CURRENT APPLICATION NUMBER: US/11/137,465
/ PRIOR FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US/10/239,663
/ PRIOR FILING DATE: 2002-09-24
/ PRIOR APPLICATION NUMBER: PCT/US01/09226
/ PRIOR FILING DATE: 2001-03-22
/ PRIOR APPLICATION NUMBER: 60/192,158
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: 60/192,668
/ PRIOR FILING DATE: 2000-03-27
/ PRIOR APPLICATION NUMBER: 60/200,166
/ PRIOR FILING DATE: 2000-04-27
```

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; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 60
; LENGTH: 189
; TYPE: PRF
; ORGANISM: Homo sapiens
US-11-137-465-60
```

```

Query Match          4.0%; Score 41; DB 7; Length 189;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 8; Mismatches 28; Indels 12; Gaps 3;
```

```

QY      61 CGGNSYSTCASCPCSPDRMKYKHCYFVSVEKDNSSLFC--LARDSHLVITDNO 117
DB      121 CCG-----TCPALNSLRHSSPECYKRAVPTCPW--LFCRCPTMTLFLSLMQDDEH 171
```

```

QY      118 EMSL 121
DB      172 KMSV 175
```

RESULT 12

```

US-11-147-492-28
; Sequence 28, Application US/11147492
; Publication No. US2005026785A1
```

GENERAL INFORMATION:

```

; APPLICANT: Kapp, Joachim-Freidrich
; APPLICANT: Kuehl, Uwe
; APPLICANT: Groetzbach, Georg
; APPLICANT: Schultheiss, Heinz-Peter
; APPLICANT: Sowade, Olaf
; APPLICANT: Stuerzebecher, Claus-Steffen
; TITLE OF INVENTION: Treatment of Cardiomyopathy and Endothelial Dysfunction
; FILE REFERENCE: 53223
; CURRENT APPLICATION NUMBER: US/11/147,492
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/579,024
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 28
; LENGTH: 189
; TYPE: PRF
; ORGANISM: homo sapiens
US-11-147-492-28
```

```

Query Match          4.0%; Score 40.5; DB 7; Length 189;
Best Local Similarity 25.6%; Pred. No. 2e+03;
Matches 31; Conservative 13; Mismatches 40; Indels 37; Gaps 6;
```

```

QY      39 VAITIGLTLAVLSVLVYMWILCOGNSYSTCASC-----SC-PDRKM 80
DB      1 MLTSSSLMAVL--VLSTYKSLGCDLPQTHSLGNRRALLLAQNGRISPSCLKDR-- 56
```

```

QY      81 KVGNCYFVSVEKDN-----SSLRFCLARDSHLVITDNO---EMSLQVFLSEA 129
DB      57 ----HDFGLPQEFPOBNQOKTOAISVLHEMIGQTFNLFSTEDSSAAMQSILKRFTEL 112
```

```

QY      130 F 130
DB      113 Y 113
```

RESULT 13

```

US-11-147-492-24
; Sequence 24, Application US/11147492
; Publication No. US2005026785A1
```

GENERAL INFORMATION:

```

; APPLICANT: Kapp, Joachim-Freidrich
; APPLICANT: Kuehl, Uwe
; APPLICANT: Groetzbach, Georg
; APPLICANT: Schultheiss, Heinz-Peter
; APPLICANT: Sowade, Olaf
```

```

; APPLICANT: Stuerzebecher, Claus-Steffen
; TITLE OF INVENTION: Treatment of Cardiomyopathy and Endothelial Dysfunction
; FILE REFERENCE: 53223
; CURRENT APPLICATION NUMBER: US/11/147,492
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US 60/579,024
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 24
; LENGTH: 189
; TYPE: PRF
; ORGANISM: homo sapiens
US-11-147-492-24
```

```

Query Match          3.8%; Score 38.5; DB 7; Length 189;
Best Local Similarity 24.6%; Pred. No. 3.2e+03;
Matches 15; Conservative 10; Mismatches 21; Indels 15; Gaps 3;
```

```

QY      85 HCYFVSVEKDNSSLRFCLARDSHLVITDNOEWSLQVFLSEAFCWIGLRNNGMRWE 144
DB      57 HDEFPOEFPOBN--QFOKA-----QAISVLHEMIGQTFNLFSTONSSA--AMD 101
```

```

QY      145 D 145
DB      102 E 102
```

RESULT 14

```

US-10-467-657-2750
; Sequence 2750, Application US/10467657
; Publication No. US20050260581A1
```

GENERAL INFORMATION:

```

; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMin99, version 1.04
; SEQ ID NO: 2750
; LENGTH: 188
; TYPE: PRF
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2750
```

```

Query Match          3.7%; Score 38; DB 6; Length 188;
Best Local Similarity 20.0%; Pred. No. 3.6e+03;
Matches 15; Conservative 14; Mismatches 14; Indels 32; Gaps 3;
```

```

QY      4 SVIYEMLELPRTAQONQNYGPOQSSSKSPSCSLVATIGL-----LTVAVLS 52
DB      32 ALIYEMLELVGAT-----CLAALLAGIAIPLAVPSIAVSALVTS 71
```

```

QY      53 VLLY-QWILCOGSNY 66
DB      72 ILIMGAMWLYFRANW 86
```

RESULT 15

```

US-10-995-561-806
; Sequence 806, Application US/10995561
; Publication No. US20050272054A1
```

GENERAL INFORMATION:

```

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
```

; TITLE OF INVENTION: DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001559
 ; CURRENT APPLICATION NUMBER: US/10/995,561
 ; CURRENT FILING DATE: 2004-11-24
 ; NUMBER OF SEQ ID NOS: 85702
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 806
 ; LENGTH: 189
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-995-561-806

Query Match 3.7%; Score 38; DB 6; Length 189;
 Best Local Similarity 35.0%; Pred. No. 3.6e+03;
 Matches 7; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 77 DRMKYGNHCYRFSVEKDW 96
 DB 29 DGMVYYANH---TEKTDW 44

Search completed: January 9, 2006, 15:56:42
 Job time : 11.7044 secs

BOOK (S. 10)

CC binding to a ligand on a target cell, by contacting the pharmaceutical
CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is mouse MAFA protein

XX Sequence 188 AA;

XX SQ

Query Match 100.0%; Score 1029; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 1,1e-102;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTYILMSLWYORIL 60
DB 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTYILMSLWYORIL 60
QY 61 CCGSDSTCSHCPSCPILMTNRNGSHCYFSMEKDWNSLKFCAKDGSHLTFPPNQGVK 120
DB 61 CCGSDSTCSHCPSCPILMTNRNGSHCYFSMEKDWNSLKFCAKDGSHLTFPPNQGVK 120
QY 121 LFGELYGDPFYWIGLRNIDGMRWEGGPAISLRLTNSLIGRCGAIHRNGLOASSCEVALQ 180
DB 121 LFGELYGDPFYWIGLRNIDGMRWEGGPAISLRLTNSLIGRCGAIHRNGLOASSCEVALQ 180
QY 181 WICKKVL 188
DB 181 WICKKVL 188

RESULT 2

AA877033

ID AAR77033 standard; protein; 188 AA.

AC AAR77033;

DT 01-FEB-1996 (first entry)

DE Mammalian mast cell function-associated antigen (MAFA).

DE Mast cell function-associated antigen; MAFA; soluble; ligand;

KW identification; screening; inflammation; inflammatory; allergy; allergic;

KW prevention.

OS Rattus rattus.

PN WO9527734-A1.

PD 19-OCT-1995.

PF 06-APR-1995; 95WO-US004258.

PR 08-APR-1994; 94TL-00109257.

PA (YEDA) YEDA RES & DEV CO LTD.

PA (RYCU/) RYCUS A.

PI Pecht I, Gutmann MD, Tal M;

DR WPI, 1995-366356/47.

DR N-PSDB; AAT01471.

PT Novel DNA encoding a mast cell function-associated antigen (MAFA) -

PT useful for screening for ligands of MAFA which are useful for prevention

PT of inflammatory and allergic reactions.

PS Claim 12; Page 37; 54pp; English.

PS A soluble form of mast cell function-associated antigen (MAFA) can be

CC produced by recombinant techniques for use in the ligand- screening

CC assay. The ligands that are identified may be used alone or in
CC combination with the MAFA to prevent inflammatory and allergic reactions

XX SQ Sequence 188 AA;

XX SQ

Query Match 81.4%; Score 838; DB 2; Length 188;
Best Local Similarity 80.7%; Pred. No. 5.2e-82;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTYILMSLWYORIL 60
DB 1 MADSSYSTLELPEAPQVODESRWKLKAVLHRPHLSRFAMVALGLTYILMSLWYORIL 60
QY 61 CCGSDSTCSHCPSCPILMTNRNGSHCYFSMEKDWNSLKFCAKDGSHLTFPPNQGVK 120
DB 61 CCGSDSTCSHCPSCPILMTNRNGSHCYFSMEKDWNSLKFCAKDGSHLTFPPNQGVK 120
QY 121 LFGELYGDPFYWIGLRNIDGMRWEGGPAISLRLTNSLIGRCGAIHRNGLOASSCEVALQ 180
DB 121 LFGELYGDPFYWIGLRNIDGMRWEGGPAISLRLTNSLIGRCGAIHRNGLOASSCEVALQ 180
QY 181 WICKKVL 187
DB 181 WICKKVL 187

RESULT 3

AA88277

ID AAW88277 standard; protein; 188 AA.

AC AAW88277;

DT 29-MAR-1999 (first entry)

DE Rat mast cell function-associated antigen (MAFA).

DE Mast cell function-associated antigen; MAFA; splice variant; rat;

KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.

OS Rattus sp.

PN WO9854209-A2.

PD 03-DEC-1998.

PF 29-MAY-1998; 98WO-GB001572.

PR 31-MAY-1997; 97GB-00011148.

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

PA Hewitt EL, Lamers MBAC, Lamont A, Williams DH;

DR WPI, 1999-059806/05.

DR N-PSDB; AAW84222.

PT New polypeptide having a sequence corresponding to human mast cell

PT function-associated antigen - useful in forming and manufacturing

PT pharmaceutical compositions in the treatment of inflammatory and allergic

PT diseases, and tumour growth.

PS Disclosure; Fig 4; 44pp; English.

PS This is the amino acid sequence of rat mast cell function-associated

CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and

CC basophils. The invention relates to cloning of the human MAFA molecule

CC (see AAW88265) and to the discovery of splice variants (see AAW88266-67)

CC of human MAPA that are not found in rat. Polypeptides and synthetic
CC peptides (see AAM8258-64) based on human MAPA and human truncated MAPA
CC and polynucleotides encoding them, can be used in methods for the
CC treatment of inflammatory and allergic diseases (e.g. rheumatoid
CC arthritis and asthma), and tumour growth
XX
XX Sequence 188 AA;

Query Match	81.4%	Score 838	DB 2	Length 188
Best Local Similarity	80.7%	Pred. NO. 5.2e-82		
Matches 151	Conservative 15	Mismatches 21	Indels 0	Gaps 0

```
QY 1 MADSSISTLELBPAPQVODSBRWKVAVLHRPHSRFPAVVALGILLVIMSLMTQRL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MADNSIYSTLELPALPBRVODSRKVKAVLHRPCVYLVWVALGILLVIMSLTYQRL 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 CCGSDSTSHCPSPCEILWTRNGSHCYFYSMEKKDNSSLKFCADKQSHLLTPPDQGVK 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CCGSGCFMKSQCSRCPNLMBRNGSHCYFYSMEKRDNSSLKFCADKQSHLLTPPDQGVN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 LFGXYLGODFYWIGLRNIDGWRMEGGPALSLRLTNSLIORCGAIHRNGIQASSCEVALQ 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 LFGXYVGEDFYWIGLRNIDGWRMEDGAPALSLTSLNSVVGKCTIHRCGIHAASSCEVALQ 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 WICKYVL 187
   |||||:|||||
Db 181 WICKYVL 187
   |||||:|||||
```

```

RESULT 4
AAE11761
ID AAE11761 standard; protein; 188 AA

```

AC AAEL1761

DT 18-DEC-2001 (first entry)

Rat mast cell function associated antigen (MAFA) protein.

KM Rat; pharmaceutical composition; mast cell function associated antigen.
KM MAFK; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
KM immunosuppressive; cytoabatic.

OS *Rattus norvegicus*.

PN WO200170805-A2.

PD 27-SEP-2001.

16-MAR-2001; 2001WO-US008596.

PR 17-MAR-2000; 2000US-0190716P.

PA (GEMI-) GEMINI SCI INC.

PI Takahashi N, Mikayama T;

DR WPI; 2001-611482/70.

DR N-PSDB; AAD18736.

PT Pharmaceutical composition for treating tumor by stimulating cytotoxic PT activity of natural killer cell or T-cell, comprises an agent that binds PT to mast cell function-associated antigen 11 and on target cell.

PS Example 1; Page 19; 49pp; English

The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical

CC composition in vitro, ex vivo or in vivo by administering the composition
CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
CC an amount sufficient to inhibit cell surface MAFI binding to the ligand
CC on the target cell. The agent or the composition is useful for treating a
CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
CC tumour cell. The invention is also useful for inhibiting an activity of
CC NK cell or a T-cell. The present sequence is rat MAFI protein
XX
XX Sequence 188 AA:
50

Query Match	81.4%	Score 838	DB 4	Length 188
Best Local Similarity	80.7%	Pred. No. 5.2e-82		
Matches 151; Conservative	15	Mismatches	21	Indels 0
				Gaps 0

```
QY 1 MADSIYSTLLELPEAPQVODESRMELKXVLRPHLSRFAMVALGLTVLMSLMYQRLI 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MADNISIYSTLELPAPRVODDSRMVYKAVLRPCVSLVWVALGLTVLMSLTYQRLI 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 CCGSDSTSCSHCPCLITLRNGSHCYFYFSMEKMOSSLKECADGSHLTFPPDQGVK 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CCGSGCFMCSQCSRCPNLMRRGSHCYFYFSMEKRDMSLTKFCADGSHLTFPPDQGVN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 LFGAYLGDDFYWIGLRNIDGWRMEGGPALSILITLSLTIQRCGAIHRNGLQASSCEVALO 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 LFGQYVGEDEFYVIGLRIDIGWRMEGDPALSLITLSNSVYQKGCTIHRCGIHAASSCEVALO 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 WICKYVL 187
      |||:|||||
Db 181 WICKYVL 187
      |||:|||||
```

RESULT 5
ADD25635
ID ADD25635 standard; protein; 189 AA.

AC ADD25635;

DT 15-JAN-2004 (first entry)

DE Binding domain-immunoglobulin fusion protein-associated protein #95.

KM Binding domain; immunoglobulin; fusion protein; cytoskeletal;
 KM antiarthritic; immunosuppressive; antidiabetic; antithyroid;
 KM neuroprotective; hinge region; immunoglobulin heavy chain;
 KM CH2 constant region; CH3 constant region; IgG1;
 KM antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
 KM malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
 KM rheumatic arthritis; myasthenia gravis; Grave's disease;
 KM type I diabetes mellitus; multiple sclerosis; autoimmune disease.

OS unidentified

PN US2003118592-A1.

PD 26-JUN-2003

25-JUL-2002; 2002US-00207655.

PR 17-JAN-2001; 2001US-0367358P.

03-JUN-2002; 2002US-0385691P. PR

PA (GENE-) GENE CRAFT INC.

PI Ledbetter JA, Hayden-

DR WPI; 2003-801317/75.

PT New binding domain-

PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.

PS Disclosure; SEQ ID NO 196; 157pp; English.

CC The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.htm?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.

XX
XX
SQ Sequence 189 AA;

Query Match 55.2%; Score 568.5; DB 7; Length 189;

Best Local Similarity 57.2%; Pred. No. 7.7e-53;

Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSIVSTLEPEAPQVQDESRRWTKAVLRPHLSRFAMVALGLTVILMSLWYQRL 60
DB 1 MTDVITYSMLEPRTAQNDYGPQKSSSRPSCSLVALALGLTAVLVSLLYQWIL 60
QY 61 CGGSDSTGSHCPSPCPIILWTRNGSHCYFYSMEKDWNSSLKFCADKGSLLTFPDNGVK 120
DB 61 CGGSVSTGASCPCPDRMKYGNHCYFYSVEKDWNSSLKFCARDSLILVTDNGWS 120
QY 121 LFGELYGDFFWIGLRNIDGMRWEGPALS-LRILNLSLQRCGAIHRNGLOASSCEVAL 179
DB 121 LQVFLSAFCWIGLRNNSGMRWEDGSPNFSRISNSFVQTGAIINRNGLOASSCEVPL 180
QY 180 QWICKKV 186
DB 181 HWVCKKV 187

RESULT 6
ADY19892
ID ADY19892 standard; protein; 189 AA.

XX ADY19892;
XX
DT 05-MAY-2005 (first entry)

XX
DE PRO polypeptide SEQ ID NO 5698.

XX Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
XX Antirheumatic; Antidiabetic; Osteopathic; Hemostatic; Antileukemic;
XX Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
XX Vincicidic; Gastrointestinal-Gen.; Antipsoriatic; Antiaesthetic;
XX Antiallergic; diagnosis.

OS Homo sapiens.

PN WO2005016962-A2.

XX 24-FEB-2005.

PF 11-AUG-2004; 2004WO-US026249.

XX 11-AUG-2003; 2003US-0493546P.

PR (GENTH) GENENTECH INC.

XX Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

DR WPI, 2005-182330/19.

PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8; SEQ ID NO 5698; 158pp; English.

CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a PRO polypeptide.

XX
XX
SQ Sequence 189 AA;

Query Match 55.2%; Score 568.5; DB 9; Length 189;

Best Local Similarity 57.2%; Pred. No. 7.7e-53;

Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSIVSTLEPEAPQVQDESRRWTKAVLRPHLSRFAMVALGLTVILMSLWYQRL 60
DB 1 MTDVITYSMLEPRTAQNDYGPQKSSSRPSCSLVALALGLTAVLVSLLYQWIL 60
QY 61 CGGSDSTGSHCPSPCPIILWTRNGSHCYFYSMEKDWNSSLKFCADKGSLLTFPDNGVK 120
DB 61 CGGSVSTGASCPCPDRMKYGNHCYFYSVEKDWNSSLKFCARDSLILVTDNGWS 120
QY 121 LFGELYGDFFWIGLRNIDGMRWEGPALS-LRILNLSLQRCGAIHRNGLOASSCEVAL 179
DB 121 LQVFLSAFCWIGLRNNSGMRWEDGSPNFSRISNSFVQTGAIINRNGLOASSCEVPL 180
QY 180 QWICKKV 186
DB 181 HWVCKKV 187

RESULT 7
AAM88265
ID AAM88265 standard; protein; 189 AA.

XX AAM88265;
XX
XX

DT 29-MAR-1999 (first entry)

DE Human mast cell function-associated antigen (MAFA).

XX Mast cell function-associated antigen; MAFA, splice variant; human;
XX inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Pepcide 7..10
 FT /note="ITIM motif"
 FT Modified-site 65..67
 FT /note="Asn is N-glycosylated"
 FT Modified-site 97..99
 FT /note="Asn is N-glycosylated"
 FT Modified-site 137..139
 FT /note="Asn is N-glycosylated"
 FT Modified-site 150..152
 FT /note="Asn is N-glycosylated"
 FT
 PN MO9654209-A2.
 XX
 PD 03-DEC-1998.
 XX
 PF 29-MAY-1998; 98WO-GB001572.
 XX
 PR 31-MAY-1997; 97GB-00011148.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Hewlett EL, Lamers MBAC, Lamont A, Williams DH;
 XX
 DR WPI; 1999-059806/05.
 XX
 DR N-PSDB; AAV84198.
 XX
 DX New polypeptide having a sequence corresponding to human mast cell
 PT function-associated antigen - useful in forming and manufacturing
 PT pharmaceutical compositions in the treatment of inflammatory and allergic
 PT diseases, and tumour growth.
 XX
 PS Disclosure; Fig 1; 44pp; English.
 XX
 PS This is the amino acid sequence of human mast cell function-associated
 CC antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAV84198)
 CC encoding human MAFA can be obtained from myelogenous leukaemic cell line
 CC KUB812 or cDNA derived from human lung tissue. The encoded protein is
 CC similar to the rat form (see AAV88277) having an intracellular domain
 CC containing a putative immunoreceptor tyrosine activation motif (ITIM) and
 CC an extracellular lectin-like domain. 2 Alternatively spliced forms (see
 CC AAV88266-67) of human MAFA have been identified. Polypeptides and
 CC synthetic peptides (see AAV88258-64) based on these truncated MAFA
 CC proteins can be used in methods for the treatment of inflammatory and
 CC allergic diseases, and tumour growth
 CC
 XX
 SQ Sequence 189 AA;

Query Match 53.3%; Score 548.5; DB 2; Length 189;
 Best Local Similarity 55.6%; Pred. No. 1.1e-50;
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MADSSIVSTLELPAPQVODSRWKLKAVLHRLPHLSRFANVALGLITVIMSLMRYRIL 60
 DB 1 MTDSVIYSMLLPRTAQNDYGPQOKSSSKSCCLVAVITGLITAVLSTVLYQWIL 60
 QY 61 CCGSKDSTGCHSPCPIILMTWNGSHCYFYSMEKKDWNSSLKFCADKSGSHLTPPDNGVK 120
 DB 61 CCGSNYSTCASCPSPRMWKKYGNHCYFVSVEEKDWNSSLEFCLADSHLVTITDQEMS 120
 QY 121 LFGELYGDQFYWIGLNRINDGWRWEGPALSL-RIITNSLIQRCGAIHRNGLQASSCEVAL 179
 DB 121 LLOVFLSEAFQWIGLNRNSGWRWEDGSPILNFSRISNSFVQTGALINKGLQASSCEVPL 180
 QY 180 QWICKKV 186
 DB 181 HGVCCKV 187

ID AAE11759 standard; protein; 189 AA.
 XX
 AC AAE11759;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human mast cell function associated antigen (MAFA) protein.
 XX
 KW Human; pharmaceutical composition; mast cell function associated antigen;
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
 KW immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200170805-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 16-MAR-2001; 2001WO-US008596.
 XX
 PR 17-MAR-2000; 2000US-0190716P.
 XX
 PA (GEMI-) GEMINI SCI INC.
 XX
 PI Takahashi N, Mikayama T;
 XX
 DR WPI; 2001-611482/70.
 XX
 DR N-PSDB; AAD18734.
 XX
 DX Pharmaceutical composition for treating tumor by stimulating cytotoxic
 PT activity of natural killer cell or T-cell, comprises an agent that binds
 PT to mast cell function-associated antigen ligand on target cell.
 XX
 PS Claim 10; Page 18; 49pp; English.
 XX
 PS The present invention relates to a pharmaceutical composition comprising
 CC an agent which specifically binds to a mast cell function associated
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA
 CC ligand and a pharmaceutically acceptable excipient. The invention is
 CC useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA
 CC binding to a ligand on a target cell, by contacting the pharmaceutical
 CC composition in vitro, ex vivo or in vivo by administering the composition
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand
 CC on the target cell. The agent or the composition is useful for treating a
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible
 CC tumour cell. The invention is also useful for inhibiting an activity of
 CC NK cell or a T-cell. The present sequence is human MAFA protein
 CC
 XX
 SQ Sequence 189 AA;

Query Match 53.3%; Score 548.5; DB 4; Length 189;
 Best Local Similarity 55.6%; Pred. No. 1.1e-50;
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MADSSIVSTLELPAPQVODSRWKLKAVLHRLPHLSRFANVALGLITVIMSLMRYRIL 60
 DB 1 MTDSVIYSMLLPRTAQNDYGPQOKSSSKSCCLVAVITGLITAVLSTVLYQWIL 60
 QY 61 CCGSKDSTGCHSPCPIILMTWNGSHCYFYSMEKKDWNSSLKFCADKSGSHLTPPDNGVK 120
 DB 61 CCGSNYSTCASCPSPRMWKKYGNHCYFVSVEEKDWNSSLEFCLADSHLVTITDQEMS 120
 QY 121 LFGELYGDQFYWIGLNRINDGWRWEGPALSL-RIITNSLIQRCGAIHRNGLQASSCEVAL 179
 DB 121 LLOVFLSEAFQWIGLNRNSGWRWEDGSPILNFSRISNSFVQTGALINKGLQASSCEVPL 180
 QY 180 QWICKKV 186
 DB 181 HGVCCKV 187

RESULT 9

AEA89021

ID AEA89021 standard; protein; 188 AA.

XX AEA89021;

DT 25-AUG-2005 (first entry)

XX Chicken MHC C-type lectin receptor, B-1ec protein.

XX Transgenic animal; disease-resistance; gene therapy; screening; B-1ec;
KM lectin; major histocompatibility complex; receptor.

XX Gallus gallus.

XX WO2005054280-A2.

XX 16-JUN-2005.

XX 03-DEC-2004; 2004WO-GB005108.

XX 05-DEC-2003; 2003GB-00028248.

XX (OXFORD BIOMEDICA UK LTD.

XX (ANIM- INST ANIMAL HEALTH.

XX Carrol M, Kaufman J, Mitrophanous K;

XX WPI; 2005-425385/43.

XX N-PSDB; AEA89020.

XX Producing transgenic animal having modified resistance to disease, by
PT introducing retrovirus having polynucleotide sequence encoding protein
PT that modifies disease resistance of animal, into cell of animal.

XX Disclosure; SEQ ID NO 8; 90pp; English.

XX The present invention relates to a method of producing transgenic animal
CC having modified resistance to a disease. The method involves introducing
CC retrovirus having polynucleotide sequence encoding protein that modifies
CC disease resistance of animal, into cell of animal. The invention is
CC useful for screening proteins capable of modifying resistance of an
CC animal to a disease, for producing transgenic bird and fish and also
CC useful in gene therapy. The present sequence is the chicken major
CC histocompatibility complex (MHC) C-type lectin receptor, B-1ec protein.
CC This sequence is used to produce a transgenic animal having modified
CC resistance to a disease.

XX Sequence 188 AA;

Query Match 15.8%; Score 162.5; DB 9; Length 188;

Best Local Similarity 24.5%; Pred. No. 6; 6e-09;

Matches 45; Conservative 29; Mismatches 89; Indels 21; Gaps 7;

QY 11 ELPEAPQVQDESRLKLVKAVLRPHLSRFPMVALGLTIVIMGLMWQRILCGSKDSTCS 70

DB 3 EYREYFHVUG-TEWSRRBSRSGACTFTLTAAVFTVLTAVAF-----AVQARQP 54

QY 71 H--CPSPCILTWRNGSHCYFSEMRKQWNSSLKRCADKSHLTFPPNQGVKLEGEYLG 127

DB 55 HQPCACQCFPDVIGRGKCYFSEDSNMTSSQNNCSALGALAVFDSMEDLSFTMRHKG 114

QY 128 QDFVITGLRNING---WRWEGGPAIS--LRILTSLIRCGAIRNGIQASSCEVALOW 181

DB 115 SSPHWVGLSR-EGKEHPMEWVNRSPISHLFQVQDGL---CAYLGDAGLSSHCARRRW 170

QY 182 ICKK 185

DB 171 VCTK 174

RESULT 10

AAU19837

ID AAU19837 standard; protein; 189 AA.

XX AAU19837;

DT 04-DEC-2001 (first entry)

XX Human novel extracellular matrix protein, Seq ID No 487.

XX Human, secreted extracellular matrix protein; immunomodulatory; Anti-HIV;

XX antitumoric; antineumatic; antisclerotic; cardiac; vascular;
KM cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic;
KM antialzheimers; immune/autoimmune disease; HIV infection; anaemia;
KM human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis;

KM cancers; hyperproliferative disorder; breast neoplasm; melanoma;

KM Sezary syndrome; Gaucher's disease; neurological diseases;

KM Alzheimer's disease; Parkinson's disease; cardiovascular disorder;

KM cardiac arrest; tachycardia; angina; infection; corneal infections;

KM wound healing; immunogen; gene therapy; antisense; food additive.

XX Homo sapiens.

XX WO20015368-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001348.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198125P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-021535P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0224519P.

XX 14-AUG-2000; 2000US-0225213P.

XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225758P.

XX 14-AUG-2000; 2000US-0225759P.

XX 18-AUG-2000; 2000US-0226279P.

XX 22-AUG-2000; 2000US-0226681P.

XX 22-AUG-2000; 2000US-0226688P.

XX 22-AUG-2000; 2000US-0227182P.

XX 23-AUG-2000; 2000US-0227099P.

XX 30-AUG-2000; 2000US-0228924P.

XX 01-SEP-2000; 2000US-0228927P.

XX 01-SEP-2000; 2000US-0229343P.

XX 01-SEP-2000; 2000US-0229344P.

XX 05-SEP-2000; 2000US-0229509P.

XX 05-SEP-2000; 2000US-0229513P.

XX 06-SEP-2000; 2000US-0230437P.

XX 06-SEP-2000; 2000US-0230438P.

XX 08-SEP-2000; 2000US-0231242P.

DB 176 LMTPEWCSK MAY 188

RESULT 11

ABBI7910

XX ABBI7910 standard; protein; 189 AA.

AC

XX ABBI7910;

DT 23-JAN-2002 (first entry)

XX

DE Human nervous system related polypeptide SEQ ID NO 6567.

XX

KW Human; nocrotropic; neuroprotective; cytosolic; dermatological; viroicide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisticking; antianaemic; antidiabetic; cancer;

KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;

KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;

KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;

KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

OS Homo sapiens.

XX

PN WO200159063-A2.

XX

PD 16-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US001334.

XX

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 26-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225577P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0231968P.

PR 12-SEP-2000; 2000US-0231969P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0233399P.

PR 14-SEP-2000; 2000US-0233400P.

PR 14-SEP-2000; 2000US-0233401P.

PR 14-SEP-2000; 2000US-0233633P.

PR 14-SEP-2000; 2000US-0233644P.

PR 14-SEP-2000; 2000US-0233655P.

PR 21-SEP-2000; 2000US-0234223P.

PR 21-SEP-2000; 2000US-0234274P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236327P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236370P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 02-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241826P.

PR 20-OCT-2000; 2000US-0242221P.

PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249218P.

DT 06-NOV-2001 (first entry)
XX
XX Human protein SEQ ID NO 1337.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00663561.
XX 20-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HSE-) HSEQ INC.
XX
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
PI Ma Y, Zhao Q, Wang D, Zhang J, Ren F, Chen R, Wang ZW,
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX MPI: 2001-476283/51.
XX N-PSDB; AAK51808.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
PT
XX
XX Claim 20; Page 3580; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78123-AAH80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAH80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
XX Sequence 188 AA;
SQ

Query Match 13.9%; Score 143.5; DB 4; Length 188;
Best Local Similarity 24.5%; Pred. No. 7,6e-07;
Matches 45; Conservative 26; Mismatches 72; Indels 41; Gaps 6;

QY 40 MVALGLTVIL-----MSLWYORL-----CCSGKD-----ST 68
DB 5 MIIISIIIVLVKVGMTLFLILFPQIFKNSNGFTTTRSYGVISQIFGSSSSSPNGFITT 64
QY 69 CSHCPSCLLWTRNGSHCYFMEKKDNSSLKFCADKGSLLTPPDNGVTLFEEYIQ 128
DB 65 RSYGVICPDWDFYQARCFPLSTSSSWNESRDFCKGKSTLAIVTPEKLFQDITDA 124
QY 129 DFYVWGL---RNIDGRWEGGALSLRILTNLSIQRCGAIHNGU-----QASSCEVALDW 181
DB 125 EKYFPIGLIYHREKGRWRWINSVFNNGVNTNONFNCART---GLTKTFDAASCDISYKR 181
QY 182 ICKK 185

DB 182 ICKK 185
||:|
||:|

RESULT 15
AAU00671
ID AAU00671 standard; protein, 188 AA.
XX
XX AAU00671;
XX
XX 07-SEP-2001 (first entry)
XX
XX Human INTERCEPT 289 form 1a polypeptide.
XX
XX Human, INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain;
KM skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte;
KM bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer;
KM anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease;
KM malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis;
KM attention deficit disorder; Crohn's disease; gastroenteritis; goitre;
KM hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism;
KM muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 7..27
FT /note= "Transmembrane domain"
FT Domain 28..188
FT /note= "Extracellular domain"
XX
XX WO200129088-A1.
XX
XX 26-APR-2001.
XX
XX 23-JUN-2000; 2000WO-US017386.
XX
XX 19-OCT-1999; 99US-00420707.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Mackay CR, Myers PS, Kiret SJ, Fraser CC, Leiby KR;
PI MPI: 2001-308477/32.
XX
XX N-PSDB; AAS00661.
XX
XX New isolated nucleic acid molecule for diagnosis, prevention, and therapy
PT of human and other animal disorder, or as modulating agent for regulating
PT cellular processes.
XX
XX Claim 8; Fig 2A-2B; 263pp; English.
XX
XX The sequence represents human INTERCEPT 289 form 1a polypeptide. This
CC protein and similar others exhibit the ability to affect growth,
CC proliferation, survival, differentiation, activity, morphology, or
CC movement/migration of, e.g. T cells and cells of the heart, liver,
CC pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph
CC node, peripheral blood leukocyte, bone marrow or thymus tissue. They can
CC be used as modulating agents for regulating cellular processes, thus, the
CC proteins and their associated nucleic acids can be used to prognosticate,
CC prevent, diagnose, or treat disorders associated with physiological
CC processes. These disorders include abnormal blood coagulation, asthma,
CC anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery
CC disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis,
CC meningitis, attention deficit disorder, Crohn's disease, gastroenteritis,
CC goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary
CC embolism and muscular dystrophy. Antibodies to disorders such as these
CC can be made by providing a polypeptide of the invention to an immuno-
XX competent vertebrate and harvesting blood or serum from the vertebrate
SQ Sequence 188 AA;

Query Match 13.9%; Score 143.5; DB 4; Length 188;

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AND AGRICULTURE
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CITY OF BOSTON

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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:16:01 ; Search time 18.3009 Seconds
(without alignments)
988.409 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSYSTLELPAPQVOD.....GLQASSCEVALQWICKVLY 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1164

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838	81.4	188	2	I59421
2	56	5.4	189	2	S23149
3	54.5	5.3	189	2	A95110
4	53.5	5.2	189	2	E64527
5	53	5.2	188	1	DUBPC2
6	53	5.2	188	2	G87336
7	52.5	5.1	189	2	T19559
8	51.5	5.0	188	2	T37454
9	51.5	5.0	189	2	G97978
10	51	5.0	189	2	T02821
11	48.5	4.7	188	2	C86508
12	48.5	4.7	188	2	H72114
13	47.5	4.6	188	1	JC2393
14	47.5	4.6	188	2	T33623
15	47.5	4.6	188	2	A72745
16	46.5	4.5	189	2	S30039
17	46	4.5	189	2	E96569
18	46	4.5	189	2	S58493
19	46	4.5	189	2	S60587
20	45.5	4.4	188	2	T17574
21	45.5	4.4	189	2	AG1997
22	45	4.4	188	2	T33027
23	45	4.4	189	2	B64209
24	45	4.4	189	2	PC1173
25	45	4.4	189	2	PC1172
26	44.5	4.3	188	2	D70820
27	44.5	4.3	188	2	A39787
28	44.5	4.3	189	2	S34632
29	44	4.3	188	2	S74560

30	44	4.3	188	2	F82587	dioxynase Xf2210
31	43.5	4.2	189	2	T00401	hypothetical prote
32	43	4.2	189	2	D84342	peptidyl-prolyl is
33	42.5	4.1	188	2	E97104	phospholipase D fa
34	42.5	4.1	188	2	AH1883	hypothetical prote
35	42.5	4.1	188	2	E88951	protein C38C3.8 (1
36	42.5	4.1	188	2	G75326	probable 16S rRNA
37	42.5	4.1	189	2	T25481	hypothetical prote
38	42.5	4.1	189	2	H86083	hypothetical prote
39	42	4.1	188	2	UC6547	high sulfur protei
40	42	4.1	188	2	T37501	hypothetical prote
41	42	4.1	189	2	G72294	conserved hypothet
42	42	4.1	189	2	B29795	circumsporozoite p
43	42	4.1	189	2	G64909	DNA packaging prot
44	42	4.1	189	2	B71542	hypothetical prote
45	42	4.1	189	2	D86909	conserved hypothet

ALIGNMENTS

RESULT 1

I59421
mast cell function associated antigen - rat

C/Species: Rattus norvegicus (Norway rat)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Jul-2004

C/Accession: I59421

R/Gutmann, M.D.; Tal, M.; Pecht, I.

Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995

A/Title: A secretion inhibitory signal transduction molecule on mast cells is another C

A/Reference number: I59421; PMID:96016176; PMID:7568140

A/Accession: I59421

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-188 <RES>

A/Cross-references: UNIPROT:Q64335; UNIPARC:UPI000030101; EMBL:X79812; NID:G1020141; P

C/Genetics:

A/Genes: mafa

Query Match 81.4%; Score 838; DB 2; Length 188;
Best local Similarity 80.7%; Pred. No. 9.2e-75;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY	1	MADSSYSTLELPAPQVODZSRWKAVLHRLPSFAMVALGLTIVIMSLTMYORTL 60
DB	1	MADSSYSTLELPAPQVODZSRWKAVLHRLPSFAMVALGLTIVIMSLTMYORTL 60
QY	61	CCGSKDSTGSHCHSCPIILMTBNGSHCYFSMEKDNSSLKFCADKSHLTFPDNQYK 120
DB	61	CCGSKDSTGSHCHSCPIILMTBNGSHCYFSMEKDNSSLKFCADKSHLTFPDNQYK 120
QY	121	LFGEYLGDPFYWIGLNNIDGMRWEGPALSLRLITNSLIRCGAHRNGLOASSCEVALQ 180
DB	121	LFGEYLGDPFYWIGLNNIDGMRWEGPALSLRLITNSLIRCGAHRNGLOASSCEVALQ 180
QY	181	WICKKYL 187
DB	181	WICKKYL 187

RESULT 2

S23149
hypothetical protein 3 (nuc 3' region) - Shigella flexneri plasmid psa

C/Species: Shigella flexneri

C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004

C/Accession: S23149

R/Close, S.M.; Kado, C.I.

Submitted to the EMBL Data Library, March 1992

A/Description: A gene near the plasmid psa origin of replication encodes a nuclease.

A/Reference number: S23149

A/Accession: S23149

A/Molecule type: DNA

A/Residues: 1-189 <CLO>

```

C:Cross-references: UNIPROT:P29772; UNIPARC:UPI000000DA3; GB:U30471; EMBL:M81325; NID:9
C:Genetics:
A:Genome: plasmid
C:Superfamily: Shigella flexneri plasmid psa hypothetical protein 3 (nuc 3' region)

Query Match          5.4%; Score 56; DB 2; Length 189;
Best Local Similarity 27.5%; Pred. No. 4,4e+02;
Matches 19; Conservative 9; Mismatches 35; Indels 6; Gaps 2;

OY      10 LELPE-APQVDESRWKIKAVLRHPHLSRFMAVLGLITVINSMLMYORILCCGSXDSST 68
       |||||:::--:-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:|-:
DB      30 LELPOLVPANNEVMWRPLVPENHPDAFWMTASNAQSDFIVYVNGIAFRWALALGVEDS- 88

OY      69 CSHCPSCPI 77
       ::::
DB      89 ----QACPL 93

RESULT 3
A95110
Acetyltransferase, GNAT family [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 31-Dec-2004
A:Accession: A95110
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A.:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95110
A:Status: preliminary
A:Molecule type: DNA
A:Reads: 1-189 <KIR>
A:Cross-references: UNIPROT:Q9JRT6; UNIPARC:UPI0000051661; GB:AEO05672; PIDN:AAK75074.1
C:Genetics:
A:Experimental source: strain TIGR4
A:Gene: SP0953
C:Superfamily: ribosomal protein serine N-acetyltransferase

Query Match          5.3%; Score 54.5; DB 2; Length 189;
Best Local Similarity 26.4%; Pred. No. 6,2e+02;
Matches 24; Conservative 16; Mismatches 38; Indels 13; Gaps 5;

OY      95 DMNSLKPCADKSGHLTFPPNOGVKLGEYLGDFFWICGRLNDGMRWGSPALSRLT 154
       :|:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      28 DAEMAFDYASKGRVTTRFTPTNQSIETKKNIAQ-FY---LANPLG-RW-----GIELK 76

OY      155 TNSLIORGAIHRNGLQASSCEVALLOWICKK 185
       :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB      77 SNG--QFIGTIDLKHKIDSVLKKALGYINK 105

RESULT 4
E64527
hypothetical protein HP0061 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
A:Accession: E64527
R:Tombl, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalek, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.W.; Fujii, C.; Bowman, C.; Wathey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpi, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: E64527
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Reads: 1-189 <TOM>
A:Cross-references: UNIPROT:O24901; UNIPARC:UPI000000C07D9; GB:AEO00528; GB:AEO00511; NID:9

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Query Match 5.2%; Score 53.5; DB 2; Length 189;
Best Local Similarity 31.9%; Pred. 7.8e+02;
Matches 23; Conservative 9; Mismatches 25; Indels 15; Gaps 4;

QY 94 KDNWSSLKFCADKGSLLTFPPDNGVK--LFGYGLGDPFYIGLARI-----DGMRW 143
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 KDNWLSLKI-EDRSNSNL-----GNGTKKLLTNADLSGDYKTYIVDSMKTYHQSQEKYKR 153
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 144 EGGPALSRLIT 155
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 154 ERGSETLEVRPT 165
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
dCMP deaminase (EC 3.5.4.12) - phage T2
N/Alternate names: deoxycytidylate deaminase
C/Species: phage T2
A/Note: host Escherichia coli
C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
A/Accession: A01011
R/Maley, G.F.; Guarino, D.U.; Maley, F.
J. Biol. Chem. 258, 8290-8297, 1983
A/Title: Complete amino acid sequence of an allosteric enzyme, T2 bacteriophage deoxycty
A/Reference number: A01011; MUID:83258442; PMID:6345541
A/Accession: A01011
A/Molecule type: protein
A/Residues: 1-188 <MAL>
A/Cross-references: UNIPROT:P00814; UNIPARC:UPI000012902B
C/Comment: The active enzyme is a hexamer of identical chains.
C/Comment: This is an allosteric enzyme whose activity is greatly influenced by the end
C/Superfamily: phage T4 dCMP deaminase
C/Keywords: allosteric regulation; hexamer; hydrolyase

Query Match 5.2%; Score 53; DB 1; Length 188;
Best Local Similarity 19.8%; Pred. No. 8.7e+02;
Matches 16; Conservative 10; Mismatches 23; Indels 32; Gaps 3;

QY 68 TCSHCPSCPIILWTRNG---SHCYRFSMEKKDNWSSLKFCADKGSLLTFPPDNGVKLFG 123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 TLSPCPDCAKAIASGGIKLVCEYDKXKPGWDDILR-----NAGIEVF- 172
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 124 EYLGDPEYWGILANIDGMWE 144
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 -----NVPKLNWE 180
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
G87336
conserved hypothetical protein CC0706 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: G87336
R/Nierman, W.C.; Deibiyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Land, M.C.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: G87336
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-188 <STO>
A/Cross-references: UNIPROT:Q9AAM0; UNIPARC:UPI0000007138; GB:AE056673; MID:G13421929; P
C/Genetics:
A/Gene: CC0706

Query Match 5.2%; Score 53; DB 2; Length 188;
Best Local Similarity 22.7%; Pred. No. 8.7e+02;
Matches 27; Conservative 7; Mismatches 35; Indels 50; Gaps 4;

QY 13 PEARPOVESRMKLVAKVLRPHLSRFAMVALGLITVILMSLWYQRIILCGSKDSTCSHC 72
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


A>Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A|Reference number: AB6491; MUID:2030349; PMID:10871362
A|Accession: C86508
A|Status: Preliminary
A|Molecule type: DNA
A|Residues: 1-188 <STO>
A|Cross-references: UNIPROT:Q9Z944; UNIPARC:UPI0000D4127; GB:AB000008; NID:g8978512; PIDN:
A|Experimental source: strain J138
C|Genetics:
A|Gene: yggE
C|Superfamily: hypothetical protein HI0304

Query Match 4.7%; Score 48.5; DB 2; Length 188;
Best Local Similarity 40.0%; Pred.No.2.4e+03;
Matches 14; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

OY 83 GSHCYFSMEKKD-WNSSLKFCADKGSHLTFPPDN 116
 | : | : | : | : | : | : | : | :
DB 150 GNKDVFYSPEEDLMALVLKDLGGKYASLTVPDN 184

RESULT 12

H72114
transcription regulator, probable CP0633 [imported] - Chlamydophila pneumoniae (strains
C|Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C|Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C|Accession: H72114; E81555
R|Katman, S.; Mitchell, W.; Martche, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.,
Nature Genet. 21, 385-389, 1999
A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A|Reference number: A72000; MUID:99206606; PMID:10192388
A|Accession: H72114
A|Molecule type: DNA
A|Residues: 1-188 <ARN>
A|Cross-references: UNIPROT:Q9Z944; UNIPARC:UPI0000D4127; GB:AE001600; GB:AE001363; NID:
A|Experimental source: Strain CHL029
R|Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1405, 2000
A>Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A|Reference number: AB1500; MUID:20150255; PMID:10684935
A|Accession: E81555
A|Molecule type: DNA
A|Residues: 1-188 <REA>
A|Cross-references: UNIPARC:UPI0000D4127; GB:AE002221; GB:AE002161; NID:g7189543; PIDN:
A|Experimental source: strain AR39, HL cells
C|Genetics:
A|Gene: yggE; CP0633
C|Superfamily: hypothetical protein HI0304

Query Match 4.7%; Score 48.5; DB 2; Length 188;
Best Local Similarity 40.0%; Pred.No.2.4e+03;
Matches 14; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

OY 83 GSHCYFSMEKKD-WNSSLKFCADKGSHLTFPPDN 116
 | : | : | : | : | : | : | : | :
DB 150 GNKDVFYSPEEDLMALVLKDLGGKYASLTVPDN 184

RESULT 13

UC2393
phospholipase A2 inhibitor 31k chain - monocled cobra
C|Species: Najia najia kaouthia, Najia najia siamensis (monocled cobra)
C|Date: 24-Feb-1995 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C|Accession: UC2393
R|Ohkura, N.; Inoue, S.; Ikeda, K.; Hayashi, K.
Biochem. Biophys. Res. Commun. 204, 1212-1218, 1994
A>Title: The two subunits of a phospholipase A2 inhibitor from the plasma of thailand co
A|Reference number: UC2393; MUID:95071456; PMID:7980598
A|Accession: UC2393
A|Molecule type: protein
A|Residues: 1-188 <OHK>
A|Cross-references: UNIPROT:O7L2I1; UNIPARC:UPI000017387C

```

A:Experimental source: plasma
A:Superfamily: Crotalus neutratizing factor; Ly-6 homolog
C:Keywords: glycoprotein; phospholipase A2 inhibitor; plasma
F:1-90/Domatin: Ly-6 homolog <Ly6>
F:1-27,6-13,20-48,54-75,76-81,99-124,117-146,150-112/Disulfide bonds: #status predicted
F:157/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match          4.6%; Score 47.5; DB 1; Length 188;
Best Local Similarity 23.2%; Pred. No. 3e+03;
Matches 32; Conservative 15; Mismatches 44; Indels 47; Gaps 8;

QY 58 RLTCGSGKSTC-----SHCPSCPIILWTRNGSHC-YFSEMEKQWNSLRFKCADKSHL 110
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 72 RLQCC--DERCEPEQPSGHCAHP-----NGYICPGIFGLFSLDSSANEAVC--KGTET 122
                                     |||  |||  |||  |||  |||  |||  |||

QY 111 LTFPDNGVKLFGEYLGODPFWIGLRNIDGRWE---GGPALSLRLITN-----SLIQR 162
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 123 KCI-----NIAGRKMEYPEDIAVYINIGICSSCEPLSLSNRT 159

QY 163 GAIRHNGLOASCEVALQ 180
   :  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 160 HEYDRNELIKVECTDAVK 177

RESULT 14
T33623
hypothetical protein F40G9.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33623
R:Graves, T.; Suterer, C.; Ozersky, P.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid F40G9.
A:Reference number: Z21378
A:Accession: T33623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-188 <R>
A:Cross-references: UNIPROT:Q9T275; UNIPARC:UP1000007BD20; EMBL:AF099919; P1DN:AA66804
A:Experimental source: strain Bristol N2, clone F40G9
C:Genetic8:
A:Gene: CESP:F40G9.10
A:Map position: 3
A:Introns: 63/3; 99/1; 113/3; 153/3

Query Match          4.6%; Score 47.5; DB 2; Length 188;
Best Local Similarity 21.3%; Pred. No. 3e+03;
Matches 19; Conservative 15; Mismatches 30; Indels 25; Gaps 5;

QY 79 WTRNGHCYFSEMEKQWNSLRFKCADKSHL--TFPDNGVKLFGEYLQ----- 128
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 54 WFSYTFPCYKSTARANFNDAHNACRSEGSLSIHSLTENO-----FLVQLSAGNR 106
                                     |||  |||  |||  |||  |||  |||  |||

QY 129 -----DFYWIGL--RNIDGRWEGPAL 150
   :  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB 107 VNSKTYVMIGLIFENRE--WSWTDGSSVN 134

RESULT 15
A72745
hypothetical protein ABE0468 - Aetopyrum pernix (strain K1)
C:Species: Aetopyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A72745
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawauchi, Y.
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aetopyrum
A:Reference number: A72450; WUID:99310339; PMID:10382966
A:Accession: A72745
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <R>

```

A; Cross-references: UNIPROT:Q9YEU3; UNIPARC:UPI000005DB7A; DDBJ:AP000059; NID:g5103911;

A; Experimental source: strain K1

C;Genetics:

A;Gene: APE0488

C:Superfamily: Aeropyrum pernix hypothetical protein APE04888

Query Match	Score	DB 2;	Length
4.6%	47;	DB 2;	188;

Best Local Similarity 29.3%; Pred. No. 3.3e+03;
Matches 22; Conservative 8; Mismatches 23; Indels 22; Gaps 5;

Matches	22;	Conservative	8;	Mismatches	23;	Indels	22;	Gaps	5
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98 SSLKFCADKG-----SHLLTFPD-NQGVKLFGE---YLGQDFYWIGLRNIDGW 141

Db 12 SSLRVLLDRGFRFTIIGGTVEYALGSRDLGDDVDLFGEEPPPLLEEYY--GVAHELGW 69

QY 142 ---RWEGGPALSLR 152

Db 70 SSGQTWLGTPRLAR 84

Search completed: January 9, 2006, 15:36:34
Job time : 20.3009 secs

Job time : 20.3009 secs

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OF
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CITY
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YORK
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IMPROVEMENT
OF
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ARTS
AND
MANUFACTURES
OF
THE
CITY
OF
NEW
YORK

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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:14:56 ; Search time 96.4956 Seconds
(without alignments)
1374.564 Million cell updates/sec

Title: US-09-811-367b-3
Perfect score: 1029
Sequence: 1 MADSSISTYLELPAPQVQD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 9256

Minimum DB seq length: 188

Maximum DB seq length: 189

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_05.80.*
2: uniprot_sprot.*
3: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029	100.0	188	088713_MOUSE	088713 mus musculu
2	838	81.4	188	064335_RAT	064335 rattus norv
3	568.5	55.2	189	075613_HUMAN	075613 homo sapien
4	548.5	53.3	189	043198_HUMAN	043198 homo sapien
5	162.5	15.8	188	062193_CHICK	062193 gallus gall
6	162.5	15.8	188	062196_CHICK	062196 gallus gall
7	143.5	13.9	188	01C5A_HUMAN	09125 homo sapien
8	143.5	13.9	188	052M11_HUMAN	052M11 homo sapien
9	135.5	13.2	189	08C634_MOUSE	08C634 mus musculu
10	109.5	10.6	189	061969_MOUSE	061969 mus musculu
11	96.5	9.4	189	060503_CAEBR	060503 caenorhabdi
12	83	8.1	188	09W012_DROME	09W012 drosophila
13	78.5	7.6	189	018202_CAEBL	018202 caenorhabdi
14	76	7.4	189	096DR9_HUMAN	096DR9 homo sapien
15	72.5	7.0	188	09W3D8_DROME	09W3D8 drosophila
16	69.5	6.8	189	086129_MYTED	086129 mytilus edu
17	69.5	6.8	189	03LM07_SILPO	03LM07 silicibacte
18	64	6.2	188	08EC21_SHEON	08EC21 shewanella
19	62	6.0	188	06N1X4_RHOPA	06N1X4 rhodospheudo
20	60.5	5.9	188	04V649_DROME	04V649 drosophila
21	57.5	5.6	188	06QJ81_HUMAN	06QJ81 homo sapien
22	57.5	5.6	188	04KBR0_PSEPF	04KBR0 pseudomonas
23	57.5	5.6	189	08NFC2_HUMAN	08NFC2 homo sapien
24	56	5.4	189	07K9P1_GAPIC	07K9P1 plasmodium
25	56	5.4	189	07K9P1_GAPIC	07K9P1 plasmodium
26	55.5	5.4	189	086EX9_SCHJA	086EX9 schistosoma
27	55.5	5.4	189	04VZ21_VIRIU	04VZ21 lassa virus
28	54.5	5.3	188	084R12_ABAAT	084R12 arabidopsis
29	54.5	5.3	189	097R76_STRPN	097R76 streptococ
30	54	5.2	188	050MR5_ENTHI	050MR5 entamoeba h
31	54	5.2	189	04RR79_TETNG	04RR79 tetradodon n

ALIGNMENTS

```

RESULT 1
088713_MOUSE PRELIMINARY; PRT; 188 AA.
AC 088713;
ID 088713_MOUSE PRELIMINARY;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Mast cell function-associated antigen 2Fl (Killer cell lectin-like
DE receptor G1) (MAFA).
GN Name=Klrg1; Synonyms=Mafa, mafa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia; Scurionath;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C.B-17 SCID;
RX MEDLINE=99077194; PubMed=9862378;
RT "2Fl antigen, the mouse homolog of the rat 'mast cell function-
RT associated antigen', is a lectin-like type II transmembrane receptor
RT expressed by natural killer cells.";
RL Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvevTACFBx; TISSUE=Spleen;
RX MEDLINE=2115136; PubMed=11220622; DOI=10.1007/s002510000282;
RT Voehringer D., Kaufmann M., Pircher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the
RT killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue
RT of MAFA.";
RL Immunogenetics 52:206-211(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99077501; PubMed=9862665;
RT Blasler C., Kaufmann M., Pircher H.;
RT "Virus-activated CD8 T cells and lymphokine-activated NK cells express
RT the mast cell function-associated antigen Mafa, an inhibitory C-type
RT lectin.";
RL J. Immunol. 161:6451-6454(1998).
RN [4]
RX EMBL; AF097357; AAD03718.1; -; mRNA.
RX EMBL; AF317727; AAK40082.1; -; Genomic DNA.
RX EMBL; AJ010751; CAA09342.1; -; mRNA.
RX HSSP; Q13241; 1B6E.
DR Ensembl; ENSMUSG00000030114; Mus musculus.
DR MGI; MGI:1355294; Klrg1.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005529; F:sugar binding; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.

```

KW Lectin; Receptor.
 FT CHAIN 2 188 mast cell function-associated antigen
 SQ SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;
 (MAFA).
 Query Match 100.0%; Score 1029; DB 2; Length 188;
 Best Local Similarity 100.0%; Pred. No. 6.6e-92;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60
 DB 1 MADSSYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60
 QY 61 CCGSDSTCSHCPSCPILMTNRNGSHCYFSEMEKDWNSSLKFCADKGSLLTFPDNGVK 120
 DB 61 CCGSDSTCSHCPSCPILMTNRNGSHCYFSEMEKDWNSSLKFCADKGSLLTFPDNGVK 120
 QY 121 LFGEYLGODFWIGLRNIDGMRWEGGPAISLRIILNSLIQRCGAIHRNGLQASCEVALQ 180
 DB 121 LFGEYLGODFWIGLRNIDGMRWEGGPAISLRIILNSLIQRCGAIHRNGLQASCEVALQ 180
 QY 181 WICKKVL 188
 DB 181 WICKKVL 188

RESULT 2
 ID Q64335_RAT PRELIMINARY; PRT; 188 AA.
 AC Q64335;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE MAPA protein (Mast cell function associated antigen).
 GN Name=Klrg1; Synonyms=MAFA, mafa;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Sprague Dawley; TISSUE=Testis;
 RX MEDLINE=97240766; PubMed=9120279;
 RA Bocsk J. P., Gutthmann M. D., Pecht I.;
 RT "Analysis of the gene encoding the mast cell function-associated
 RT antigen and its alternatively spliced transcripts.";
 RT J. Immunol. 158:3235-3243(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96016176; PubMed=7568140;
 RA Gutthmann M. D., Tai M., Pecht I.;
 RT "A secretion inhibitory signal transduction molecule on mast cells is
 RT another C-type lectin.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
 DR EMBL; X97191; CAA65829.1; -; Genomic_DNA.
 DR EMBL; X79812; CAA65208.1; -; mRNA.
 DR EMBL; X97192; CAA65829.1; JOINED; Genomic_DNA.
 DR EMBL; X97193; CAA65829.1; JOINED; Genomic_DNA.
 DR EMBL; X97194; CAA65829.1; JOINED; Genomic_DNA.
 DR EMBL; X97195; CAA65829.1; JOINED; Genomic_DNA.
 DR PIR; I59421; I59421.
 DR HSSP; P26718; 1KCG.
 DR Ensembl; ENSRNOC0000014918; Rattus norvegicus.
 DR RGD; 61978; Klrg1.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C_1.
 DR SMART; SM00034; CLECT_1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 188 AA; 21356 MW; ZCC8032D4D020B15 CRC64;

Query Match 81.4%; Score 838; DB 2; Length 188;

Best Local Similarity 80.7%; Pred. No. 2.6e-73;
 Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60
 DB 1 MADSSYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60
 QY 61 CCGSDSTCSHCPSCPILMTNRNGSHCYFSEMEKDWNSSLKFCADKGSLLTFPDNGVK 120
 DB 61 CCGSGFWCSCCSCPNLMMENNGSHCYFSEMEKDWNSSLKFCADKGSLLTFPDNGVN 120
 QY 121 LFGEYLGODFWIGLRNIDGMRWEGGPAISLRIILNSLIQRCGAIHRNGLQASCEVALQ 180
 DB 121 LFOEYVGEDFWIGLRNIDGMRWEGGPAISLISNSVYVRCGTIHRGLHASCEVALQ 180
 QY 181 WICKKVL 187
 DB 181 WICKKVL 187

RESULT 3
 ID Q75613_HUMAN PRELIMINARY; PRT; 189 AA.
 AC Q75613;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE ITIM-containing receptor MAF-L (Mast cell function-associated antigen
 DE homolog).
 GN Name=MAFA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99057052; PubMed=9842918;
 RX DOI=10.1002/(SICI)1521-4141(199811)28:11<3755::AID-IMMU3755>3.0.CO;2-3;
 RA Butcher S., Arney K.L., Cook G.P.;
 RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene
 RT complex and expressed by basophils and NK cells.";
 RT Eur. J. Immunol. 28:3755-3762(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99077194; PubMed=9862378;
 RA Hanke T., Corral L., Vance R.E., Pauls D.H.;
 RT "2F1 antigen, the mouse homolog of the rat 'mast cell function-
 RT associated antigen', is a lectin-like type II transmembrane receptor
 RT expressed by natural killer cells.";
 RT Eur. J. Immunol. 28:4409-4417(1998).
 DR EMBL; AF081675; AAC32200.1; -; mRNA.
 DR EMBL; AF097358; AAD03719.1; -; mRNA.
 DR HSSP; Q13241; 1B6E.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C_1.
 DR SMART; SM00034; CLECT_1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 KW Receptor.
 SQ SEQUENCE 189 AA; 21206 MW; FA9023F1523656A8 CRC64;

Query Match 55.2%; Score 568.5; DB 2; Length 189;
 Best Local Similarity 57.2%; Pred. No. 4.4e-47;
 Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

QY 1 MADSSYSTLELPEAPQVQDESRLKAVLHRPHLSRFAMVALGLTIVLMSLTYORIL 60
 DB 1 MTDSTVYEMLELPRTAQDQNYGPOQSSSSSRSCCVALLGLTIVLMSLTYORIL 60
 QY 61 CCGSDSTCSHCPSCPILMTNRNGSHCYFSEMEKDWNSSLKFCADKGSLLTFPDNGVK 120

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Db 61 COG5N5TSCASCSPDRMWTGNNHCYYSVEEKDNSSLFCLARDSHLVTITNOEMS 120
Qy 121 LFGELYGDFWYIGLNRIDGMWEGGPAISL-RIITNSLIORCGAIHRNGLOASSCEVAL 179
Db 121 LIAQVFLSEAFWIGLNNSGMRWEDSPINFSRISSNIVQTCGALINKGLOASSCEVPL 180
Qy 180 QWICKKV 186
Db 181 HWICKKV 187

RESULT 4
ID 043198 HUMAN PRELIMINARY; PRT; 189 AA.
AC 043198;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mast cell function-associated antigen.
DE Name=MAFA;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Enzyme digested lung;
RX MEDLINE=9843875; PubMed=9765598; DOI=10.1016/S0167-4781(98)00107-9;
RT Lamers M.B., Lamont A.G., Williams D.H.;
RT "Human MAFA has alternatively spliced variants."
RL Biochim. Biophys. Acta 1399:209-212(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Enzyme digested lung;
RA Lamers M.B.A.C., Lamont A.G., Williams D.H.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF034952; AAC34731.1; -; mRNA.
DR HSSP; Q13241; 1B6E.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR GO; GO:0004872; F: receptor activity; TAS.
DR GO; GO:0005529; F: sugar binding; TAS.
DR GO; GO:0007166; P: cell surface receptor linked signal transdu. . .; TAS.
DR GO; GO:0006968; P: cellular defense response; TAS.
DR GO; GO:0006954; P: inflammatory response; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLCCT; 1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 189 AA; 21075 MW; 15B042AD40B2B4F6 CRC64;

Query Match 53.3%; Score 548.5; DB 2; Length 189;
Best Local Similarity 55.6%; Pred. No. 3.9e-45;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
```

```
Qy 1 MADSSISTELPAPPOVODESRWKLKAVLHRPHLSRFAMVALGLTVILMSLIMYORIL 60
Db 1 MTBVTITSMLEPLRITAOANDYRPOQKSSSSKSCSCVATLTGLTRAVLISVLLYQWIL 60
Qy 61 CCGSKDSTCTSHCPSCPIILWTRNGSHCYYSMEKKDNMSLKFCAADKSGHLLTPPDNOCVK 120
Db 61 CGGNSYSTSCASCSPDRMWTGNNHCYYSVEEKDNSSLFCLARDSHLVTITNOEMS 120
Qy 121 LFGELYGDFWYIGLNRIDGMWEGGPAISL-RIITNSLIORCGAIHRNGLOASSCEVAL 179
Db 121 LIAQVFLSEAFWIGLNNSGMRWEDSPINFSRISSNIVQTCGALINKGLOASSCEVPL 180
Qy 180 QWICKKV 186
Db 181 HWICKKV 187

RESULT 6
ID 06ZYP6 CHICK PRELIMINARY; PRT; 188 AA.
AC 06ZYP6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE B-1ec protein.
DE Name=B-1ec;
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RX PubMed=15749883;
RA Rogers S.L., Gobel T.W., Vierthoeck B.C., Milne S., Beck S.,
RA Kaufman J.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT reveals that the NK Complex and the MHC share a common ancestral
RT region."
RT J. Immunol. 174:3475-3483(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RA Rogers S.L.;
RT "Characterisation of C-type lectin-like receptors in the chicken
RT MHC."
RT Thesis (2002), Department of Pathology and Microbiology, University of
RL Bristol, Bristol, United Kingdom.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bursa;
RA Kaufman J.F.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ634337; CG25421.1; -; mRNA.
DR HSSP; Q9H8F0; 1K9J.
DR GO; GO:0005529; F: sugar binding; ISA.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTI-FREEZE1.
DR SMART; SM00034; CLCCT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN_1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SQ SEQUENCE 188 AA; 21053 MW; 6AD5AC3C9BB8F440 CRC64;

Query Match 15.8%; Score 162.5; DB 2; Length 188;
Best Local Similarity 24.5%; Pred. No. 1.4e-07;
Matches 45; Conservative 29; Mismatches 89; Indels 21; Gaps 7;
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE B-1ec protein.
GN Name=B-1ec;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Bone marrow;
RX PubMed=1579983;
RA Rogers S.L., Gobel T.W., Viertlboeck B.C., Milne S., Beck S.,
RA Kautman J.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT reveals that the NK complex and the MHC share a common ancestral
RT region.";
RL J. Immunol. 174:3475-3483 (2005).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Bone marrow;
RA Rogers S.L.;
RT "Characterisation of C-type lectin-like receptors in the chicken
RT MHC.";
RL Theiss (2002), Department of Pathology and Microbiology, University of
RL Bristol, Bristol, United Kingdom.
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Bone marrow;
RA Kautman J.F.;
RT Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ634334; CACG25418.1; -; mRNA.
DR HSPF; Q9H8F0; 1K9J.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; Antifreeze11.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C_1;
DR PRINTS; PR00356; ANTI-FREEZE11.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 188 AA; 20997 MW; 9FD5BD2D9BF9FE41 CRC64;

Query Match 15 8%; Score 162.5; DB 2; Length 188;
Beet Local Similarity 24.5%; Pred. No. 1,4e-07;
Matches 45; Conservative 29; Mismatches 89; Indels 21; Gaps 7;

OY 11 ELPEAPQVQDESRRKLVKAVLRPHLSRFPMVALGLTVLMSLWYQRIICGSKDSTCS 70
DB 3 ERYREYFHYVG-TEWGRRRBSPSGACVTQITMAAFTVILITAVAF-----AQAQAP 54
OY 71 H--CPSPFILTNRNGSHCYFSMERKQWSSLKFCADKSHLLTFPDNGVKLGEYLG 127
DB 55 HPQPCAQCQCFWIDIGFRGKCYFSEDSNMTSSQNNCSALGASLAVFDSAEIDLSFTMRKG 114
OY 128 QDFYVIGLRLNDG----WRMEGPHLS--LRITLSLILORCAIHRNGIQASSCEVALQW 181
DB 115 SSPHWVAGLSR-EGKEHAWEMVNRSPSLHFLVOVGDL---CAVLADAGLSSSHCARRW 170
OY 182 ICKK 185
DB 171 VCTK 174

RESULT 7
CLCSA HUMAN STANDARD; PRT; 188 AA.
AC Q9NY25; Q9UKO0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)

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```

DE C-type lectin domain family 5 member A (C-type lectin superfamily
DE member 5) (Myeloid DAP12-associating lectin) (MDL-1).
DE Name=CLECSA; Synonyms=CLECSF5, MDL1;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), FUNCTION, TISSUE SPECIFICITY,
RP INTERACTION WITH TYROBP, AND MOTILGENESIS OF LYS-16.
RX MEDLINE=99380598; PubMed=10449773; DOI=10.1073/pnas.96.17.9792;
RA Bakker A.B.H., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;
RT "Myeloid DAP12-associating lectin (MDL)-1 is a cell surface receptor
RT involved in the activation of myeloid cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796 (1999).
[2]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Mueller A., Merz H., Feller A.C.;
RT "Expression of MDL-1 in human blood and cell lines.";
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., Oloughlin M.D., Schaller M.E.,
RA Fewell G.A., Delhanty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., All J., Andrews S., Isak A.,
RA Vandrunt A., Nguyen C., Du P., Lamar B., Courtney J., Kalicki J.,
RA Ozerky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Mink P., Maupin R., Stromatt C.,
RA Lacroille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendi M.C., Yang S.-P., Schultz B.R., Wallis J.W., Speith J.,
RA Biert L.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendinning J., Kaul R., Kent W.J., Frey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Filcek P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164 (2003).
-1- FUNCTION: May be involved in proinflammatory activation of myeloid
CC cells via TYROBP-mediated signaling in a calcium-dependent manner.
CC -1- SUBUNIT: Interacts with TYROBP.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NY25-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NY25-2; Sequence=VSP_012839;
CC -1- TISSUE SPECIFICITY: Expressed in peripheral blood monocytes and in
CC the monocyte/macrophage cell lines U937 and MonoMac6, but not in
CC cell lines of other origins. Expression is down-regulated when
CC monocytes differentiate into dendritic cells.
CC -1- SIMILARITY: Contains 1 C-type lectin domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF139768; AA02491.1; -; mRNA.
CC EMBL; AJ271684; CAB71334.1; -; mRNA.
CC EMBL; AC073647; AAS07444.1; -; Genomic_DNA.
CC HSPF; P22897; IREG.

```

DR Ensembl, ENSG00000090269, Homo sapiens.
 DR HGNC, HGNC:2054, CLEC5A.
 DR MIM, 604987, -, C: integral to plasma membrane; TAS.
 DR GO, GO:0005887, C: integral to plasma membrane; TAS.
 DR GO, GO:0005488, F: binding; TAS.
 DR GO, GO:0005686, P: cellular defense response; TAS.
 DR GO, GO:0007165, P: signal transduction; TAS.
 DR InterPro, IPRO02353, AntifreezeZell.
 DR InterPro, IPRO01304, Lectin_C.
 DR Pfam, PF00059, Lectin_C, 1.
 DR PRINTS, PR00356, ANTI-FREEZE1.
 DR SMART, SM00034, CLECT, 1.
 DR PROSITE, PS00615, C-TYPE LECTIN 1, FALSE_NEG.
 DR PROSITE, PS50041, C-TYPE LECTIN 2, 1.
 DR KMW, Alternative splicing, Glycoprotein, Immune response, Lectin;
 KW Signal-anchor, Transmembrane.
 FT TOPO_DOM 1 4 Cytoplasmic (Potential).
 FT TRANSMEM 5 27 protein-anchor for type II membrane
 FT TOPO_DOM 28 188 Extracellular (Potential).
 FT DOMAIN 78 184 C-type lectin.
 FT CARBOHYD 32 32 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 93 93 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 144 144 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 151 151 N-linked (GLCNAC. . .) (Potential).
 FT DISULFID 71 82 By similarity.
 FT DISULFID 99 183 By similarity.
 FT DISULFID 161 175 Missing (in isoform 2).
 FT VARSPIC 116 116 /FTId=VSP_012839.
 FT MUTAGEN 16 16 K->I: Abolishes interaction with TYROBP.
 SQ SEQUENCE 188 AA, 21521 MW, 94A2DBD520DC1985 CRC64;
 Query Match 13.9%; Score 143.5; DB 1; Length 188;
 Best Local Similarity 24.5%; Pred. No. 1e-05;
 Matches 45; Conservative 26; Mismatches 72; Indels 41; Gaps 6;
 40 MVALGLTVL-----MSLMYQRI-----CCGSKD-----ST 68
 5 MIISGLIVLVKVGWTLFLYFPQIFNKNDGFTTTSYGVTSQIFGSSSPNGFIT 64
 69 CSHCPSCPILWTRNGSHCYFYSMEKKDWNSSLFKCADKSHLTFPDNGVXLFGEYLQ 128
 65 RSYGVCPKDMERYQRCFFLSTSSSWNESRDFCKGKSTLAIIVTPKLFLODITDA 124
 QY 129 DFYWIGL---RNIDGRMEGPPALSLRLITNSLIQRCGAIHRNGL---QASSCEVALQW 181
 DB 125 EKYFTGLIYHREKRWKRWNNNSVFNNGVNTNQNFCATL---GLTKTFDASCDISYR 181
 QY 182 ICKK 185
 DB 182 ICKK 185
 QY 182 ICKK 185
 DB 182 ICKK 185
 RESULT 8
 052M11_HUMAN PRELIMINARY; PRT; 188 AA.
 ID 052M11_HUMAN PRELIMINARY; PRT; 188 AA.
 AC 052M11_HUMAN PRELIMINARY; PRT; 188 AA.
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE C-type lectin, superfamily member 5.
 DE Name=CLEC5A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung and heart;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge U.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Roark S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Shevchenko Y., Bouffard G.G.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein U.E., Jones S.J.W., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung and heart;
 RG NIH MGC Project;
 RL Submitted (Apr-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL, BC093714; AAH93714.1; -, mRNA.
 KW Lectin.
 SQ SEQUENCE 188 AA, 21521 MW, 94A2DBD520DC1985 CRC64;
 Query Match 13.9%; Score 143.5; DB 2; Length 188;
 Best Local Similarity 24.5%; Pred. No. 1e-05;
 Matches 45; Conservative 26; Mismatches 72; Indels 41; Gaps 6;
 40 MVALGLTVL-----MSLMYQRI-----CCGSKD-----ST 68
 5 MIISGLIVLVKVGWTLFLYFPQIFNKNDGFTTTSYGVTSQIFGSSSPNGFIT 64
 69 CSHCPSCPILWTRNGSHCYFYSMEKKDWNSSLFKCADKSHLTFPDNGVXLFGEYLQ 128
 65 RSYGVCPKDMERYQRCFFLSTSSSWNESRDFCKGKSTLAIIVTPKLFLODITDA 124
 QY 129 DFYWIGL---RNIDGRMEGPPALSLRLITNSLIQRCGAIHRNGL---QASSCEVALQW 181
 DB 125 EKYFTGLIYHREKRWKRWNNNSVFNNGVNTNQNFCATL---GLTKTFDASCDISYR 181
 QY 182 ICKK 185
 DB 182 ICKK 185
 QY 182 ICKK 185
 DB 182 ICKK 185
 RESULT 9
 08C634_MOUSE PRELIMINARY; PRT; 189 AA.
 ID 08C634_MOUSE PRELIMINARY; PRT; 189 AA.
 AC 08C634_MOUSE PRELIMINARY; PRT; 189 AA.
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:4922502D21 product:hypothetical C-type lectin domain
 DE containing protein, full insert sequence (Similar to C lectin-related
 DE protein A).
 GN Name=4922502D21Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RX NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).


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Db      61 NKTCDDEVKLCPKDNKLRQNCFSRIQKNSWLTANDICELDATALVFIKTEVEILMN 120
Qy      124 EYLGGDFVYIGH--RNIDG-WPEEGGPAISLRILNLSL--IQ---RCGAIHRNGLOASSC 175
      : ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121 QIQEMKTYWIGLHRQNLGIMWTNWSK-----NNLHIEDHQGCAVHKKGIDSTSC 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      176 EVALQWICKK 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      175 EDQKEPCTCR 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
Q61969 MOUSE PRELIMINARY; PRT; 189 AA.
ID 061969
AC 061969
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE Natural killer cell receptor-PI (Fragment).
GN Name=NKR-PI 34;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRATN-BALB/c;
RX MEDLINE=92388663; PubMed=1517565;
RA Giorda R., Weisberg E.P., Ip T.K., Trucco M.;
RT "Genomic structure and strain-specific expression of the natural
RT killer cell receptor NKR-PI."
RL J. Immunol. 149:1957-1963(1992).
DR EMBL; X64719; CAA45972.1; -, mRNA.
DR HSSP; Q07108; 1FMS.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR Interpro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.
DR Receptor.
KW NON_TER
FT NON_TER 1
SQ SEQUENCE 189 AA; 21310 MW; D60584BD967073B0 CRC64;

Query Match
Best Local Similarity 23.4%; Score 109.5; DB 2; Length 189;
Matches 40; Conservative 24; Mismatches 72; Indels 35; Gaps 8;

Qy      23 RWKLVKAVLRPHLSRFAMVNLGLTVILMSLLM-----YORICCGSKDST---C 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      27 RW-----HRLAL-KFGCAGILLVVLTGCVLVSVQSSVVKICADVQENRTHTTDC 79
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      70 SHCPSCPIIWRNNGSHCYFSEMEKDWNSLKFCAKDGSHLLTPPDNGVTLFGSEYLGQD 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      80 SVNLECPQDWLSHMDKCFRVPQVNTWEEGQADGKCAATLLIQQDEELRFLDLSIEK 139
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      130 F--YWIGLRNI--DGMWEEGPAISLRILNLSIQCGAIHRNGLOASSC 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      140 YNSFWIGLRFTLPDMWKMINGTTF-----NSDVLKITGVTEG---SC 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
Q60S03 CAEBR PRELIMINARY; PRT; 189 AA.
ID 060S03
AC 060S03
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein CBG20753 (Fragment).
GN Name=CBG20753;
OS Caenorhabditis briggsae.

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OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodetidae; Caenorhabditis.
OC NCBI_Taxid=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX The C. briggsae Sequencing Consortium;
RT Submitted (SEP-2003) to the EMBL/Genbank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAC0100115; CAE73324.1; -, Genomic_DNA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR Interpro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 189
SQ SEQUENCE 189 AA; 21805 MW; 48F6021C793C4845 CRC64;

Query Match
Best Local Similarity 9.4%; Score 96.5; DB 2; Length 189;
Matches 49; Conservative 26; Mismatches 61; Indels 67; Gaps 12;

Qy      4 SSTYSTLELPEAP-QVQD-ESRWKLVKAVLRPHLSRFAMVNLGLTVILMSLLMYQRIIC 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      27 NSFFSTDE--EFPYQNFGRTOYRIKREKVERLETVG-----LQSTIME----- 75
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      62 CSKSKSTCHSCSPILM--TRNGSHCYFSEMEKDWNSLKFCAKDGSHLLTPPDNGV 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      76 -----MNVTEGSK-YRFFPERKNWDAEKGCOFGAHLAII-DNEAK 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      120 KLFGGYL-----GQDFYIGLR-----NIDGRMGGPAISLRILNLSIQNC 162
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      117 NFEVTVLINSSETPAWIGMTKTSQTSTPTFTFD-----SESPIDGC 161
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      163 GAIRNGCL-QASSCEVALQWICK 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      162 AVVDSKGVWSIRSCIQLRPPVQ 184
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 12
Q9W012 DROME PRELIMINARY; PRT; 188 AA.
ID Q9W012
AC Q9W012
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE CG9134-PA, isoform A (CG9134-pc, isoform c) (R15266P).
GN ORFNames=CG9134;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_Taxid=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotlier P.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Butler A.,
RA Burlis K.C., Buzam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Chew J.S., Dahlke C., Davaport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Garibollian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaisli M., Katush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laaso P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Mikhina N.V., Mobarry C., Morris J., Moshirei A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Rehner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang R.A., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kamlirker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D.N.-J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RG Flybase, (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkeley;

RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
 RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL, AE003471; AAF47464.1; -; Genomic_DNA.
 DR EMBL, BT012477; AA593748.1; -; mRNA.
 DR HSSP, P08661; 1BV4.
 DR Ensemble; CG9134; *Drosophila melanogaster*.
 DR Flybase; FBgn003199; CG9134.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C_1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN_1.
 DR PROSITE; PS00411; C TYPE LECTIN 2; 1.
 SQ SEQUENCE 188 AA; 21848 MW; 51B6C20B2C039DE CRC64;

Query Match 8.1%; Score 83; DB 2; Length 188;
 Best local similarity 19.7%; Pred. No. 7.8;
 Matches 36; Conservative 31; Mismatches 66; Indels 50; Gaps 10;

QY 49 ILMSLWYQRLTCCGSK-----DSTCHCPSC-----PILWT-----RNGSHCYFF 89
 DB 5 LILSVILQLCLIDRTMATPKGPGVADCPNCVDSEQYTPNKMTPPLKLGKRYLL 64
 QY 90 SM-EKKDWNSSLRKCADKSHLTTPDQ-----GVKLFGEYLGDFFWIG----- 134
 DB 65 GIPFAMWFKATQYCRHYGMHLASISQGEENDRLKHKIRDP--LGHHFWIISGTDLADE 122
 QY 135 -----LNIDGWRWEGPALSIRITNSLIRCGAI-HRNG---LQASSCVALQW 181
 DB 123 GNFFWMTATGRITFTNNMAGEPNNFR-YENGEBCLELWNRDGLKWNDSPCSFEYTF 181
 QY 182 ICK 184
 DB 182 VCE 184

RESULT 13
 018202 CAEEL PRELIMINARY; PRT; 189 AA.
 AC 018202;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Hypothetical protein Y48B1B.9.
 GN ORFNames=Y48B1B.9;
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; *Caenorhabditis*.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018 (1998).
 RL EMBL; Z93393; CAB07697.2; -; Genomic_DNA.
 DR PIR; T27020; T27020.
 DR HSSP; P22030; 1FVU.
 DR WormBase; WBGene0013008; Y48B1B.9.
 DR WormDep; Y48B1B.9; CE36239.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C_1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00411; C TYPE LECTIN 2; 1.
 DR PROSITE; PS00411; C TYPE LECTIN 2; 1.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 189 AA; 21548 MW; 192DA964586072FO CRC64;

Query Match 7.6%; Score 78.5; DB 2; Length 189;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:25:12 ; Search time 25.2885 Seconds
(without alignments)
614.628 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029
Sequence: 1 MADSSYSTLELPEAPQVOD.....GLQASSCEVALQWICKVLY 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 991

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5.COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6.COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H.COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUS.COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE.COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	838	81.4	188	2	US-08-722-126A-5
2	838	81.4	188	4	PCT-US95-04258-5
3	52	5.1	188	2	US-09-543-681A-7232
4	51.5	5.0	188	2	US-09-902-540-12348
5	51.5	5.0	189	1	US-08-469-427A-15
6	49.5	4.8	189	2	US-09-248-796A-19356
7	48.5	4.7	188	2	US-09-438-185A-957
8	47	4.6	189	2	US-09-438-185A-339
9	46.5	4.5	188	1	US-08-905-267-2
10	46.5	4.5	188	2	US-09-314-051-2
11	46.5	4.5	188	2	US-09-617-389B-2
12	44.5	4.3	188	1	US-07-749-001-5
13	44.5	4.3	188	1	US-08-154-198-5
14	44.5	4.3	188	1	US-08-463-335-5
15	44.5	4.3	188	1	US-08-464-033A-5
16	44	4.3	188	2	US-09-134-000C-3652
17	43.5	4.2	188	2	US-09-252-991A-29925
18	43.5	4.2	188	2	US-09-438-185A-761
19	43.5	4.2	189	2	US-09-198-452A-549
20	43	4.2	188	2	US-09-122-443-14
21	43	4.2	188	2	US-07-757-022B-32
22	43	4.2	188	2	US-09-558-089-14
23	43	4.2	188	2	US-09-558-087-14
24	43	4.2	188	2	US-09-248-796A-20257
25	43	4.2	188	2	US-09-558-474-14
26	42.5	4.1	188	2	US-09-252-991A-30309
27	42.5	4.1	188	2	US-09-605-703B-1580

28	42	4.1	188	2	US-08-858-207A-497	Sequence 497, App
29	42	4.1	189	2	US-09-902-540-16146	Sequence 16146, A
30	42	4.1	189	2	US-09-949-016-10489	Sequence 10489, A
31	41.5	4.0	188	2	US-09-252-991A-28935	Sequence 28935, A
32	41.5	4.0	188	2	US-09-270-767-38256	Sequence 38256, A
33	41.5	4.0	188	2	US-09-270-767-53473	Sequence 53473, A
34	41.5	4.0	189	2	US-09-270-767-45559	Sequence 45559, A
35	41	4.0	188	2	US-09-500-569-8	Sequence 8, Appl1
36	41	4.0	188	2	US-09-971-823B-8	Sequence 19379, A
37	41	4.0	188	2	US-09-248-796A-19379	Sequence 19379, A
38	41	4.0	189	6	5171685-2	Patent No. 5171685
39	41	4.0	189	6	5518916-2	Patent No. 5518916
40	40.5	3.9	188	2	US-09-636-215-592	Sequence 592, App
41	40.5	3.9	188	2	US-09-685-166A-592	Sequence 592, App
42	40.5	3.9	188	2	US-09-679-426-592	Sequence 592, App
43	40.5	3.9	188	2	US-09-759-143-592	Sequence 592, App
44	40.5	3.9	188	2	US-09-651-236-592	Sequence 592, App
45	40.5	3.9	188	2	US-09-657-279-592	Sequence 592, App

ALIGNMENTS

```

RESULT 1
US-08-722-126A-5
; Sequence 5, Application US/08722126A
; Patent No. 6034227
; GENERAL INFORMATION:
; APPLICANT: PECHT, Israel
; APPLICANT: GUTTMANN, Marcelo D.
; APPLICANT: TAL, Michael
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,126A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PECHT=1A
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-722-126A-5
; Query Match 81.4%; Score 838; DB 2; Length 188;
; Best Local Similarity 80.7%; Pred. No. 4e-86;

```


Db 73 LLDGIAFGFNVVDLPILASRLRCPVAVWRPPDDAVERALR 116

RESULT 5

US-08-469-427A-15

Sequence 15, Application US/08469427A

Patent No. 5607918

GENERAL INFORMATION:

APPLICANT: Eriksson, Ulf

APPLICANT: Olofsson, Birgitta

APPLICANT: Alltalo, Kari

APPLICANT: Pajusola, Katri

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND

TITLE OF INVENTION: DNA CODING THEREFOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan

STREET: 1200 G Street, N.W., Suite 700

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,427A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/397,651

FILING DATE: 01-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Evans, Joseph D

REGISTRATION NUMBER: 26,269

REFERENCE/DOCKET NUMBER: 41979cp2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-8800

TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 189 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-469-427A-15

Query Match 5.0%; Score 51.5; DB 1; Length 189;

Best Local Similarity 28.1%; Pred. No. 1.2e+03;

Matches 16; Conservative 8; Mismatches 22; Indels 11; Gaps 2;

Db 21 ESRWKLAVLRPHLSRFAMVAGLTLVTLMSILMYRILCCGSKDSTC--SHCPSC 75
97 ESNITMIMRKPKQSGH-----IERWSFLQHRRCRCPKDKTKPENHCEPC 144

RESULT 6

US-09-248-796A-19356

Sequence 19356, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074, 725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 19356

LENGTH: 189

TYPE: PRT

ORGANISM: Candida albicans

FEATURE:

NAME/KEY: UNSURE

LOCATION: (184), (185)

OTHER INFORMATION: Identity of amino acid sequences at the above locations are unk

US-09-248-796A-19356

Query Match 4.8%; Score 49.5; DB 2; Length 189;

Best Local Similarity 27.3%; Pred. No. 2e+03; 24; Indels 31; Gaps 5;

Matches 24; Conservative 9; Mismatches 24; Indels 31; Gaps 5;

Db 93 KKDWSLKFCDKSGSHL--LTFPDNGVKLFG--EYGDGFYWIGLRNIDGWRWEGP 147
102 KLTYSFLQNCRTNHTMAQINFCKSAVELFGINETLG---YGVGFYV----- 149

Db 148 ALSRLITNSLIQRCGAIH-RNGLOASS 174
150 -----ROLAHLRNSINATS 164

RESULT 7

US-09-438-185A-957

Sequence 957, Application US/09438185A

Patent No. 6822071

GENERAL INFORMATION:

APPLICANT: Stephens, Richard

APPLICANT: Mitchell, Wayne

APPLICANT: Kaiman, Sue

APPLICANT: Davis, Ronald

TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

FILE REFERENCE: 018941-000411US

CURRENT APPLICATION NUMBER: US/09/438, 185A

CURRENT FILING DATE: 2002-03-13

PRIOR APPLICATION NUMBER: US 60/108, 279

PRIOR FILING DATE: 1998-11-12

PRIOR APPLICATION NUMBER: US 60/128, 606

PRIOR FILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 1074

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 957

LENGTH: 188

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

FEATURE:

OTHER INFORMATION: CPN0955

US-09-438-185A-957

Query Match 4.7%; Score 48.5; DB 2; Length 188;

Best Local Similarity 23.5%; Pred. No. 2.6e+03;

Matches 16; Conservative 11; Mismatches 20; Indels 21; Gaps 3;

Db 78 LMTNRGSHCYFYFMEKKDWSLKFCDKSGSHLTL-----FPDNGV---KLF 122
15 LGSRRNRKRCGFF-----FSSGTALGKGRGHEHLPSTIKLHKKHYVLYLDHGGIPTEKAY 68

Db 123 GEYLGDPF 130
69 QSLLPDGY 76

RESULT 8

US-09-438-185A-339

Sequence 339, Application US/09438185A

Patent No. 6822071

GENERAL INFORMATION:

APPLICANT: Stephens, Richard

APPLICANT: Mitchell, Wayne

APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 189
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
FEATURE:
OTHER INFORMATION: CPN0337
US-09-438-185A-339

Query Match 4.6%; Score 47; DB 2; Length 189;
Best Local Similarity 29.4%; Pred. No. 3.9e+03;
Matches 15; Conservative 10; Mismatches 20; Indels 6; Gaps 2;

QY 21 ESRWTKAVLRPHSRF-AMVALGLTVITLMSLMYQ-----RLCCGSK 65
DB 112 EERRRKLILHRYELRLEKGLAOGKMTILPLGMLSRGYVVRIGCCRGK 162

RESULT 9
US-08-905-267-2
Sequence 2, Application US/08905267
Patent No. 5959075
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Conklin, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Lofton-Day, Catherine E.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,267
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-905-267-2

Query Match 4.5%; Score 46.5; DB 1; Length 188;
Best Local Similarity 30.8%; Pred. No. 4.4e+03;
Matches 20; Conservative 7; Mismatches 17; Indels 21; Gaps 5;

QY 60 LCCGSKDSTGCHSPCLMTWRNSHCYFSMEKKDNNSLKFCADKSHLLTFPDNGV 119
DB 4 LCC-----SC-LLWL--GILLAPFSQOEVTSPYKLC---GRDLIV---EVI 42

QY 120 KLFGF 124
DB 43 KLCCG 47

RESULT 10
US-09-314-051-2
Sequence 2, Application US/09314051
Patent No. 6183991
GENERAL INFORMATION:
APPLICANT: Lok, Si
APPLICANT: Conklin, Darrell C.
APPLICANT: Adams, Robyn L.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Lofton-Day, Catherine E.
TITLE OF INVENTION: TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,051
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-314-051-2

Query Match 4.5%; Score 46.5; DB 2; Length 188;
Best Local Similarity 30.8%; Pred. No. 4.4e+03;
Matches 20; Conservative 7; Mismatches 17; Indels 21; Gaps 5;

QY 60 LCCGSKDSTGCHSPCLMTWRNSHCYFSMEKKDNNSLKFCADKSHLLTFPDNGV 119
DB 4 LCC-----SC-LLWL--GILLAPFSQOEVTSPYKLC---GRDLIV---EVI 42

QY 120 KLFGF 124
DB 43 KLCCG 47

RESULT 11
US-09-617-389B-2

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/ Sequence 2, Application US/09617389B
/ Patent No. 6709659
/ GENERAL INFORMATION:
/ APPLICANT: Lok, Si
/ APPLICANT: Conklin, Darrell C.
/ APPLICANT: Lofton-Day, Catherine E.
/ TITLE OF INVENTION: Antibodies That Bind Testis-Specific
/ FILE REFERENCE: 96-06C3
/ CURRENT APPLICATION NUMBER: US/09/617,389B
/ CURRENT FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 09/339,148
/ PRIOR FILING DATE: 1999-06-24
/ PRIOR APPLICATION NUMBER: 08/905,267
/ PRIOR FILING DATE: 1997-01-18
/ PRIOR APPLICATION NUMBER: 60/023,213
/ PRIOR FILING DATE: 1996-02-08
/ PRIOR APPLICATION NUMBER: 60/031,592
/ PRIOR FILING DATE: 1996-11-21
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FaastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ US-09-617-389B-2

Query Match
Best Local Similarity 30.8%; Pred. No. 4.4e+03;
Matches 20; Conservative 7; Mismatches 17; Indels 21; Gaps 5;

QY 60 LCCGSKDSTCHSPCPILWTRNGSHCYPSMEKQWNSLKFCDKSHLLTFPPNGV 119
Db 4 LCC-----SC-LFWL--GLLAPRSGQGEVTSPTKLC--GRDLLV----EVI 42

QY 120 KLFGE 124
Db 43 KLCQG 47

RESULT 12
US-07-749-001-5
/ Sequence 5, Application US/07749001
/ Patent No. 5264557
/ GENERAL INFORMATION:
/ APPLICANT: Salomon, David S.
/ APPLICANT: Persico, Maria G.
/ TITLE OF INVENTION: A HUMAN CRYPTO-RELATED GENE
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CUSHMAN, DABY & CUSHMAN
/ STREET: 1615 L Street, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/749,001
/ FILING DATE: 19910823
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Scott, Watson T.
/ REGISTRATION NUMBER: 26,581
/ REFERENCE/DOCKET NUMBER: WTS/5683/91630/SRL
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 861-3000
/ TELEFAX: (202)822-0944
/ TELEX: 248453 CUSH
```

```
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 188 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-07-749-001-5

Query Match
Best Local Similarity 25.0%; Pred. No. 7.3e+03;
Matches 18; Conservative 10; Mismatches 29; Indels 15; Gaps 4;

QY 19 QDSRWKAKVALRPHLSRFAMVALGLTVILMSLMYQRI--LCCGSKDSTC---SHCP 73
Db 47 RDDSIMPOEPAIRPSSQ-----RVLPMGIQHSKELNRTCC-LNEGTCMLGSCFCA 96

QY 74 SCPILWTRNGSH 85
Db 97 CPPSPFYGRNCEH 108

RESULT 13
US-08-154-198-5
/ Sequence 5, Application US/08154198
/ Patent No. 5620866
/ GENERAL INFORMATION:
/ APPLICANT: SALOMON, David S.
/ APPLICANT: PERSICO, Maria G.
/ TITLE OF INVENTION: A HUMAN CRYPTO-RELATED GENE
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: Stewart Street Tower, One Market Plaza
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: US
/ ZIP: 94105-1493
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/154,198
/ FILING DATE: 17-NOV-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION NUMBER: 435
/ APPLICATION NUMBER: US 07/749,001
/ FILING DATE: 23-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Baetlian, Kevin L.
/ REGISTRATION NUMBER: 34,774
/ REFERENCE/DOCKET NUMBER: 15280-63-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 188 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-154-198-5

Query Match
Best Local Similarity 25.3%; Score 44.5; DB 1; Length 188;
Matches 18; Conservative 10; Mismatches 29; Indels 15; Gaps 4;

QY 19 QDSRWKAKVALRPHLSRFAMVALGLTVILMSLMYQRI--LCCGSKDSTC---SHCP 73
Db 47 RDDSIMPOEPAIRPSSQ-----RVLPMGIQHSKELNRTCC-LNEGTCMLGSCFCA 96

QY 74 SCPILWTRNGSH 85
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Db 97 CPSPFYGRNCEH 108

RESULT 14

US-08-463-335-5
Sequence 5, Application US/08463335
Patent No. 5650285
GENERAL INFORMATION:
APPLICANT: Salomon, David S.
TITLE OF INVENTION: A HUMAN CRYPTO-RELATED GENE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,335
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,001
FILING DATE: 23-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/91630/SRL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 248453 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-335-5

Query Match 4.3%; Score 44.5; DB 1; Length 188;

Best Local Similarity 25.0%; Pred. No. 7.3e+03;

Matches 18; Conservative 10; Mismatches 29; Indels 15; Gaps 4;

QY 19 QDESHWKAKAVLHRLPHLSRFAMVALGLTILMSLMTYORI--LCCGSKDSTC---SHCP 73

Db 47 RDDSIMPOEPAIRPRSSQ-----RVLPWGIOHSKEINRTCC-INBGTCLMGSFCA 96

QY 74 SCPIILWTRNGSH 85

Db 97 CPSPFYGRNCEH 108

RESULT 15

US-08-464-023A-5
Sequence 5, Application US/08464023A
Patent No. 5854339
GENERAL INFORMATION:
APPLICANT: Salomon, David S.
TITLE OF INVENTION: A Human Cripco-Related Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,023A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,001

FILING DATE: 23-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/154,198

FILING DATE: 17-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 15280-63-1-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 188 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-464-023A-5

Query Match 4.3%; Score 44.5; DB 1; Length 188;

Best Local Similarity 25.0%; Pred. No. 7.3e+03;

Matches 18; Conservative 10; Mismatches 29; Indels 15; Gaps 4;

QY 19 QDESHWKAKAVLHRLPHLSRFAMVALGLTILMSLMTYORI--LCCGSKDSTC---SHCP 73

Db 47 RDDSIMPOEPAIRPRSSQ-----RVLPWGIOHSKEINRTCC-INBGTCLMGSFCA 96

QY 74 SCPIILWTRNGSH 85

Db 97 CPSPFYGRNCEH 108

Search completed: January 9, 2006, 15:38:00
Job time : 26.2885 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 9, 2006, 15:35:43 ; Search time 72.5361 Seconds
(without alignments)
1082.906 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSISTYLELPEAPQVOD.....GLQASSCEVALQWICKKVLV 188

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 6603

Minimum DB seq length: 188

Maximum DB seq length: 189

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications, AA, Main:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	100.0	188	US-09-811-367B-3	Sequence 3, Appli
2	838	81.4	188	US-09-811-367B-5	Sequence 5, Appli
3	568.5	55.2	189	US-10-207-655-196	Sequence 156, App
4	568.5	55.2	189	US-10-756-149-5210	Sequence 5210, Ap
5	548.5	53.3	189	US-09-811-367B-1	Sequence 1, Appli
6	152	14.8	189	US-09-764-870-487	Sequence 487, App
7	152	14.8	189	US-10-125-540-487	Sequence 487, App
8	143.5	13.9	188	US-09-759-130B-83	Sequence 83, Appl
9	143.5	13.9	188	US-10-287-436A-69	Sequence 69, Appl
10	143.5	13.9	188	US-10-287-436A-1251	Sequence 1251, Ap
11	143.5	13.9	188	US-11-097-143-5490	Sequence 5490, Ap
12	83	8.1	188	US-11-097-143-3261	Sequence 3261, Ap
13	72.5	7.0	188	US-10-114-893-48	Sequence 48, Appl
14	69.5	6.8	189	US-10-425-115-345243	Sequence 345243,
15	61.5	6.0	188	US-10-424-599-250285	Sequence 250285,
16	59.5	5.8	188	US-10-767-701-56009	Sequence 56009, A
17	56.5	5.5	188	US-10-437-963-302199	Sequence 302199,
18	56	5.4	188	US-10-424-599-260240	Sequence 260240,
19	55.5	5.4	188	US-10-424-599-260240	Sequence 1876, Ap
20	54.5	5.3	189	US-10-472-928-1876	Sequence 190542,
21	54	5.2	188	US-10-437-963-190542	Sequence 248, App
22	53.5	5.2	189	US-09-895-913A-248	Sequence 37926, A
23	52.5	5.1	189	US-10-450-763-37926	Sequence 37926, A
24	52	5.1	188	US-09-738-626-4950	Sequence 4950, Ap
25	52	5.1	189	US-10-108-260A-3303	Sequence 3303, Ap
26	52	5.1	189	US-10-767-701-34822	Sequence 34822, A
27	51.5	5.0	188	US-10-424-599-157696	Sequence 157696,

28	51.5	5.0	188	US-10-450-763-32442	Sequence 32442, A
29	51.5	5.0	189	US-10-424-599-226112	Sequence 226112,
30	51.5	5.0	189	US-10-767-701-37569	Sequence 37569, A
31	51	5.0	188	US-10-767-701-43351	Sequence 43351, A
32	50	4.9	189	US-10-074-566-66	Sequence 66, Appl
33	50	4.9	189	US-10-074-566-74	Sequence 74, Appl
34	49.5	4.8	188	US-10-389-586-909	Sequence 909, App
35	49	4.8	188	US-09-798-889-130	Sequence 130, App
36	49	4.8	188	US-10-633-680-130	Sequence 130, App
37	49	4.8	188	US-10-424-599-152847	Sequence 152847,
38	49	4.8	188	US-10-424-599-235426	Sequence 235426,
39	49	4.8	188	US-10-424-599-270985	Sequence 270985,
40	49	4.8	188	US-10-425-114-38940	Sequence 38940, A
41	49	4.8	189	US-10-425-115-242970	Sequence 242970,
42	48.5	4.7	188	US-10-425-115-315785	Sequence 315785,
43	48.5	4.7	189	US-10-501-282-1558	Sequence 1558, Ap
44	48	4.7	188	US-10-767-701-50982	Sequence 50982, A
45	48	4.7	188	US-10-425-115-308045	Sequence 308045,

ALIGNMENTS

```
RESULT 1
US-09-811-367B-3
; Sequence 3, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Miyakawa, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-811-367B-3

Query Match      100.0%; Score 1029; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 7, 6e-98;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSISTYLELPEAPQVODSRWKLKAVLHPRHLSRFAMVALGLTLVILMSILMTORIL 60
   |||||
Db 1 MADSSISTYLELPEAPQVODSRWKLKAVLHPRHLSRFAMVALGLTLVILMSILMTORIL 60

QY 61 CCSSKSTCHGCHSCPTLWTRNGSHCYFSEMEKKDNSSLKFCADKSHLLTPPDNGVK 120
   |||||
Db 61 CCSSKSTCHGCHSCPTLWTRNGSHCYFSEMEKKDNSSLKFCADKSHLLTPPDNGVK 120

QY 121 LFGELYGDYVYVGLRIIDGMRWEGPALSIRLITNSLIORCGAIHNGLOASSCEVALQ 180
   |||||
Db 121 LFGELYGDYVYVGLRIIDGMRWEGPALSIRLITNSLIORCGAIHNGLOASSCEVALQ 180

QY 181 WICKKVLV 188
   |||||
Db 181 WICKKVLV 188

RESULT 2
US-09-811-367B-5
; Sequence 5, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
```

```

; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5
```

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Query Match      81.4%; Score 838; DB 3; Length 188;
Best Local Similarity 80.7%; Pred. No. 4e-78;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
```

```

QY      1 MADSSITSTLELPEAPQVODESRWKLKAVLHRLPHLSRFAMVALGLITVIMSLMYORIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MADNSITSTLELPAAPRVQDDSRMKVKAVLHRCVSYVMVALGLITVIMSLLYORTL 60

QY      61 CCGSKDSTCSHCPCPIILMTNRGSHCYFYSMEKMDWNSLKFCAKDGSHLLTFPDNOGVK 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 CCGSGKFMCSOCSCPCPNLMNRGSHCYFYSMEKRWNSLKFCAKDGSHLLTFPDNOGVN 120

QY      121 LFGELYGODFWYIGLRNIDGWRWEGGPAALSLRLTNSLIORCGAIHRNGLOASSCEVALQ 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121 LFGELYGDEFWYIGLRNIDGWRWEGDPAALSLSLTNSVYQKGTIHRGGLHASSCEVALQ 180

QY      181 WICKCKVL 187
      |||:||||
DB      181 WICKCKVL 187
```

```

RESULT 3
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196
```

```

Query Match      55.2%; Score 568.5; DB 4; Length 189;
Best Local Similarity 57.2%; Pred. No. 2.7e-50;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;
```

```

QY      1 MADSSITSTLELPEAPQVODESRWKLKAVLHRLPHLSRFAMVALGLITVIMSLMYORIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MTDSSITSMLELPTATQANDYGPQOKSSSRPSCCLVALMALGLITVALSLVLYQWIL 60

QY      61 CCGSKDSTCSHCPCPIILMTNRGSHCYFYSMEKMDWNSLKFCAKDGSHLLTFPDNOGVK 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 CCGSNYSTCASCPCPDRMKKYGNNHCYFYSVEKMDWNSLKFCLARDSHLLVITDNOGMS 120

QY      121 LFGELYGODFWYIGLRNIDGWRWEGGPAALSLRLTNSLIORCGAIHRNGLOASSCEVAL 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121 LQVFLSEAFWCWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180
```

```

QY      180 QWICKKV 186
      |||:||||
DB      181 HWCKKV 187
```

```

RESULT 4
US-10-756-149-5210
; Sequence 5210, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5210
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5210
```

```

Query Match      55.2%; Score 568.5; DB 5; Length 189;
Best Local Similarity 57.2%; Pred. No. 2.7e-50;
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;
```

```

QY      1 MADSSITSTLELPEAPQVODESRWKLKAVLHRLPHLSRFAMVALGLITVIMSLMYORIL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MTDSSITSMLELPTATQANDYGPQOKSSSRPSCCLVALMALGLITVALSLVLYQWIL 60

QY      61 CCGSKDSTCSHCPCPIILMTNRGSHCYFYSMEKMDWNSLKFCAKDGSHLLTFPDNOGVK 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 CCGSNYSTCASCPCPDRMKKYGNNHCYFYSVEKMDWNSLKFCLARDSHLLVITDNOGMS 120

QY      121 LFGELYGODFWYIGLRNIDGWRWEGGPAALSLRLTNSLIORCGAIHRNGLOASSCEVAL 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121 LQVFLSEAFWCWIGLRNNSGMRWEDGSPINFSRISNSFVOTCGAINKGLQASSCEVPL 180

QY      180 QWICKKV 186
      |||:||||
DB      181 HWCKKV 187
```

```

RESULT 5
US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uaki
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1
```

```

Query Match      53.3%; Score 548.5; DB 3; Length 189;
Best Local Similarity 55.6%; Pred. No. 3.1e-48;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;
```

```

QY      1  MADSSYSTLELPEAPQVQDSRNKTLXVLRPHLSRFAMVALGILTVILMSLMTQRII. 60
Db      1  MTDVIVYSMELPTATQANDYGPOQKSSSSSKPSCICVAILTGLVAVLSTVLYOMIL. 60
QY      61  CCSGKSDTSCSPSCPIILMTRNGSHCYFYSMEKKDMNSLKFCDKSGHLLTFPDNGVK. 120
Db      61  CGSNYSTCACPCPSCPRMKYGNHCYFYSVEKDMNSLFCCLARDSHLLVITDNGMS. 120
QY      121  LFGELYGDFYWIGLRNIDGMRWEGGPAISL-RIITNSLIORCGAIHRNGIQAASCEVAL. 179
Db      121  LLAQFLSEAFQWIGLRNNSGMRWEDGSPINFSRIENSFVQTCGAINRNGIQAASCEVPL. 180
QY      180  QWICKV 186
Db      181  HGVCCKV 187

RESULT 6
US-09-764-870-487
; Sequence 487, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 487
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-487

Query Match      14.8%; Score 152; DB 3; Length 189;
Best Local Similarity 22.3%; Pred. No. 2,7e-07;
Matches 43; Conservative 30; Mismatches 80; Indels 40; Gaps 6

QY      2  ADSSYSTLELPEAP----QVQDSRNKTLKAVLRPHLSRFAMVALGILTVILMSLMTQ. 57
Db      30  SSTAVALALELVDPPGCRNSARDEGSTSKALB----- 63
QY      58  RILCCGSKDSTCSHCPSCPIILMTRNGSHCYFYSMEKKDMNSLKFCDKSGHLLTFPDN. 116
Db      64  -----ASKG-CIKCEAPCPEDMWLXGRKCYFSESEPRPMWNTGROYCHTHBAVLAVIQSO. 116
QY      117  OGVLKFGELYGDFYWIGLRNIT-DGMRWEGGPAISLRIITNSLIORCGAIHRNGIQAASCE. 175
Db      117  KLELEFQFKTRRE-PWIGLRVQDBFPMVNGDPFDEFTIAGPGEVPEPTRLVSTEC. 175
QY      176  EVALQWICKVLY 188
Db      176  IMTRPWCCKMAY 188

RESULT 7
US-10-125-540-487
; Sequence 487, Application US/10125540
; Patent No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 487
; LENGTH: 189
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-10-125-540-487

Query Match      14.8%  Score 152;  DB 4;  Length 189;
Best Local Similarity 22.3%  Pred. No. 2,7e-07;
Matches 43;  Conservative 30;  Mismatches 80;  Indels 40;  Gaps 6;

OY 2  ADSSVSTLTLPAP-----QVDESRWKAKAVLHRPHLSRFAMVAVLGLTLVILMSLLMYQ 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 30  SSTRVAAALVLVPPGCRNARNARDEGSTWKAAL----- 63
OY 58  RILCCGSKDSTGCHSP-CPILWTRNGSHCYFSMEKQWNSLKFCAKDGSHLLTFPDN 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64  ----ASKG--CIKCEAPCEDWILGRKCYFSEPPDMWNTGRQYCHTHEAVLAVIOGQ 116
OY 117  QGVTLFSEYIGQDFYWTGLFNT--DGKRWEGCPALSLRILTNSLIQKGAIHRYGLQASSC 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 117  KELEFMKFTFRRE-PWIGLRVGDDEPHWVNDPDPDPTFIAGPGCVFVEPRIVSTEC 175
OY 176  EVALQWICKKVLV 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 176  LMTRPWVCSKMY 188

RESULT 8
US-09-759-130B-83
; Sequence 83, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCauley, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirsch, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-535ONMIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens

```



```
/ CURRENT APPLICATION NUMBER: US/10/287,436A
/ CURRENT FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: US 60/336,220
/ PRIOR FILING DATE: 2001-10-31
/ NUMBER OF SEQ ID NOS: 1446
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 1251
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-436A-1251

Query Match      13.9%; Score 143.5; DB 5; Length 188;
Best Local Similarity 24.5%; Pred. No. 2e-06;
Matches 45; Conservative 26; Mismatches 72; Indels 41; Gaps 6;

QY      40 MALGLITVIL-----MSLMYQRL-----CCGSKD-----ST 68
DB      5 MIIISGLIVVLLKVMGNTLFLYPPQIFKNSDGFTRSYGVTSQIFGSSSPSPNGFIT 64
QY      69 GSHCPSCPILTNRNGSHCYFYSMEKKDMNSLKFCAKGSHTLTFPDNGVYKLFGEYLQ 128
DB      65 RSYGVCPDMEYQARCFPLTSSESNBSRDFCKGKSTLAIYVTPPKTKFLQDITDA 124
QY      129 DFTYIGL---RNIDGRWEGGPAISLRILTNLSLQRCGAIHRNGL---QASSCEVALQW 181
DB      125 EXYFILLIYHREKRWIRWINSVFNQNTNQNFCAT---GLTKTFDASCDISYR 181
QY      182 ICKK 185
DB      182 ICEK 185

RESULT 12
US-11-097-143-5490
/ Sequence 5490, Application US/11097143
/ Publication No. US20050208558A1
/ GENERAL INFORMATION:
/ APPLICANT: Ventec, J. Craig
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/11/097,143
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: 60/157,832
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/160,191
/ PRIOR FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: 60/161,932
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 5490
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-11-097-143-5490

Query Match      8.1%; Score 83; DB 6; Length 188;
Best Local Similarity 19.7%; Pred. No. 3.6;
Matches 36; Conservative 31; Mismatches 66; Indels 50; Gaps 10;
```

```
QY      49 IILSLMYQRLICGSK-----DSTCSHCPSC-----PIIWT-----RNGSHCYF 89
DB      5 LILSVIISLQCLLDRTMATPPKGPVADCPNCDVDSQYTPNKTWPLKLGKRRYLL 64
QY      90 SM-EKKDMNSLKFCAKGSHTLTFPDNQ-----GYKLFGEYLQDFTYIG----- 134
DB      65 GIFFKAMFKATQYCRYGKMHLAGISSQENDRLKHIRDFG--LGHEHFWISGTDLADE 122
QY      135 -----LRNIDGRWEGGPAISLRILTNLSLQRCGAI-HRNG-----LQASSCEVALQW 181
DB      123 GNFPWMTATGPITFTNNMAGBPNR- YENGSEENCLIEIMWMDGKXKNDSPCSFETVF 181
QY      182 ICK 184
DB      182 VCE 184

RESULT 13
US-11-097-143-3261
/ Sequence 3261, Application US/11097143
/ Publication No. US20050208558A1
/ GENERAL INFORMATION:
/ APPLICANT: Ventec, J. Craig
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/11/097,143
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: 60/157,832
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/160,191
/ PRIOR FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: 60/161,932
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 3261
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-11-097-143-3261

Query Match      7.0%; Score 72.5; DB 6; Length 188;
Best Local Similarity 18.9%; Pred. No. 43;
Matches 25; Conservative 24; Mismatches 52; Indels 31; Gaps 7;

QY      79 WTRNGSHCYFYS-MEKKDMNSLKFCAKGSHTLTFPDNGVYKLFGEYL-----GODFY 131
DB      48 FVRIGDNYTYIEPMNKVNFQAGACQMMNAHLASIEDKPEWALLIKIMAKGFKNDYF 107
QY      132 WI-----GLRINDGWR-----WEGGPAISLRILTNLSLQRCGAIH-----RNLQQA 172
DB      108 WISGNDLGTGATYMNNSNGRPMTYAPWNGPKQMPDNYGV---ENC--VHMFAFREWIND 162
QY      173 SSCEVALQWICK 184
DB      163 ANCKIQMLYVCE 174

RESULT 14
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US-10-114-893-48
; Sequence 48, Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-48

Query Match 6.8%; Score 69.5; DB 4; Length 189;
Best Local Similarity 23.7%; Pred. No. 89;
Matches 27; Conservative 20; Mismatches 36; Indels 31; Gaps 5;

QY 3 DSSIVSTLELPE-----APQVDESRLKAVLHRLPRLSRFAMVALGLITVIMSLMYQ 57
DB 93 EASQSENEILKEMITLARKLNKSKSQWE--LHHQNLN-----LQETL--K 135
QY 58 RILCGSMDSTGSHCPSPILWTRNGSHCYFSPMEKXDMNSLKFCAKGSHTL 111
DB 136 RVANCSA-----PCQDWIMHGENCYLFGSGSPNWEKSKQKCLSLDAXLL 180

RESULT 15
US-10-425-115-345243
; Sequence 345243, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345243
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_78028C.1.pep
US-10-425-115-345243

Query Match 6.0%; Score 61.5; DB 4; Length 189;
Best Local Similarity 20.9%; Pred. No. 66+02;
Matches 24; Conservative 23; Mismatches 41; Indels 27; Gaps 5;

QY 16 PQVDESRLKAVLHRLPRLSRFAMVALGLITVIMSLMYQRIIC-----CGSK 65
DB 5 PLLSLGWSIRSA--SAPWYLGFCITLALAPRLIVDLVAIFLFQKLCSPMLISNTGAV 62

QY 66 DSTC-----SHCPSPILWTRNGSHCYFSPME-KDMNSLKFCA 105
DB 63 PCLCGEFLYMAKTAQANCDACQVLDVKEPPSHHSCVEQANYNERRRGA 117

Search completed: January 9, 2006, 15:55:59
Job time : 73.5381 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:36:43 ; Search time 10.6478 Seconds
(without alignments)
149.666 Million cell updates/sec

Title: US-09-811-367b-3

Perfect score: 1029
Sequence: 1 MADSSITSLLEAPQVQD.....GLQASSCEVALQWICKIVLY 188Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 97

Minimum DB seq length: 188
Maximum DB seq length: 189Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029	100.0	188	US-10-055-877-205	Sequence 205, App
2	838	81.4	188	US-10-055-877-206	Sequence 206, App
3	568.5	55.2	189	US-10-055-877-207	Sequence 207, App
4	548.5	53.3	189	US-10-055-877-209	Sequence 209, App
5	56	5.4	189	US-10-416-384-1	Sequence 1, Appl
6	42	4.1	188	US-10-842-206-40	Sequence 40, Appl
7	42	4.1	188	US-10-980-459-32	Sequence 32, Appl
8	41.5	4.0	188	US-10-945-853-2	Sequence 2, Appl
9	40.5	3.9	188	US-10-467-657-2750	Sequence 2750, App
10	40.5	3.9	188	US-10-131-826A-240	Sequence 240, App
11	40.5	3.9	189	US-10-467-657-246	Sequence 246, App
12	40.5	3.9	189	US-10-467-657-2690	Sequence 2690, App
13	37.5	3.6	188	US-10-945-853-1	Sequence 1, Appl
14	37	3.6	188	US-10-821-234-1393	Sequence 1393, Appl
15	37	3.6	188	US-10-528-031-4	Sequence 4, Appl
16	37	3.6	189	US-10-131-826A-232	Sequence 232, App
17	37	3.6	189	US-10-467-657-250	Sequence 6250, App
18	37	3.6	189	US-11-137-465-60	Sequence 60, Appl
19	36.5	3.5	188	US-11-064-774A-117	Sequence 117, Appl
20	35.5	3.4	189	US-11-100-183-61	Sequence 61, Appl
21	34	3.3	188	US-10-980-388-101	Sequence 101, Appl
22	34	3.3	189	US-10-793-626-2976	Sequence 2976, App
23	34	3.3	189	US-10-793-626-3000	Sequence 3000, App
24	34	3.3	189	US-10-467-657-4044	Sequence 4044, App
25	34	3.3	189	US-11-147-492-14	Sequence 14, Appl

26	33.5	3.3	188	US-10-884-730-88	Sequence 88, Appl
27	33.5	3.3	188	US-10-884-730-294	Sequence 294, App
28	33.5	3.3	188	US-10-884-730-332	Sequence 332, App
29	33.5	3.3	188	US-10-793-626-2698	Sequence 2698, App
30	33.5	3.3	189	US-10-995-561-643	Sequence 643, App
31	33.5	3.3	189	US-10-873-528-15	Sequence 15, Appl
32	33	3.2	188	US-11-036-797-37	Sequence 37, Appl
33	33	3.2	189	US-11-147-492-24	Sequence 24, Appl
34	32.5	3.2	188	US-10-821-234-941	Sequence 941, Appl
35	32.5	3.2	189	US-11-205-103-33	Sequence 33, Appl
36	32	3.1	188	US-11-000-463-866	Sequence 866, App
37	32	3.1	188	US-11-000-463-867	Sequence 867, App
38	32	3.1	189	US-10-485-517-221	Sequence 221, App
39	32	3.1	189	US-10-467-657-932	Sequence 922, App
40	32	3.1	189	US-11-147-492-12	Sequence 12, Appl
41	31.5	3.1	189	US-11-147-492-6	Sequence 6, Appl
42	31	3.0	189	US-10-821-234-1421	Sequence 1421, App
43	30.5	3.0	189	US-11-147-492-22	Sequence 22, Appl
44	30	2.9	188	US-10-980-388-90	Sequence 90, Appl
45	30	2.9	188	US-10-467-657-3200	Sequence 3200, App

ALIGNMENTS

RESULT 1
US-10-055-877-205
; Sequence 205, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Andrews, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patnirajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taulier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055, 877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262, 892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263, 598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263, 799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264, 117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264, 139
; PRIOR FILING DATE: 2001-01-25

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; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 205
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-055-877-205
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Query Match      100.0%; Score 1029; DB 6; Length 188;
Best Local Similarity 100.0%; Pred. No. 1,3e-104;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MADSSISTLELPEAPQVODESRMKLKAVALHRPHLSRFAMVALGLITVILMSLMTYQRL 60
DB      1 MADSSISTLELPEAPQVODESRMKLKAVALHRPHLSRFAMVALGLITVILMSLMTYQRL 60
QY      61 CCGSDSTCSHCPCSPILMTNRGSHCYFFSMKKDMNSSLKFCADKSGHLLTFPNOGVK 120
DB      61 CCGSDSTCSHCPCSPILMTNRGSHCYFFSMKKDMNSSLKFCADKSGHLLTFPNOGVK 120
QY      121 LFGEYLGODFYWIGLRNIDGWRMEGPGALSLRLTNSLIQRCGAIHRNGLOASSCEVALQ 180
DB      121 LFGEYLGODFYWIGLRNIDGWRMEGPGALSLRLTNSLIQRCGAIHRNGLOASSCEVALQ 180
QY      181 WICKKVLV 188
DB      181 WICKKVLV 188

RESULT 2
US-10-055-877-206
; Sequence 206, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patuturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eiseen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkens, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
```

```
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 206
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-055-877-206
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Query Match      81.4%; Score 838; DB 6; Length 188;
Best Local Similarity 80.7%; Pred. No. 6.7e-84;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
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QY      1 MADSSISTLELPEAPQVODESRMKLKAVALHRPHLSRFAMVALGLITVILMSLMTYQRL 60
DB      1 MADSSISTLELPEAPQVODESRMKLKAVALHRPCVSYLVAMVALGLITVILMSLMTYQRL 60
QY      61 CCGSDSTCSHCPCSPILMTNRGSHCYFFSMKKDMNSSLKFCADKSGHLLTFPNOGVK 120
DB      61 CCGSGKGFWCSCSCSPILMTNRGSHCYFFSMKKDMNSSLKFCADKSGHLLTFPNOGVN 120
QY      121 LFGEYLGODFYWIGLRNIDGWRMEGPGALSLRLTNSLIQRCGAIHRNGLOASSCEVALQ 180
DB      121 LFOEYVGEDEFYWIGLRNIDGWRMEGPGALSLRLTNSLVQKCGTIIHRCGLHASSCEVALQ 180
QY      181 WICKKVL 187
DB      181 WICKKVL 187

RESULT 3
US-10-055-877-207
; Sequence 207, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Rattelli, Luca
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
```



```

GENERAL INFORMATION:
Publication No. US2005028824A1

APPLICANT: Decristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratekli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Patlurajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eilsen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 209
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-209

Query Match      53.3%; Score 548.5; DB 6; Length 189;
Best Local Similarity 55.6%; Pred. No. 1,6e-52;
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1

OY      1 MADSSTSTLTELPEAPQVODESRWKLKAVLRPHLSRFAMVALGHLVIILMSLTMYORIL 60
Db      1 MTSQSVIYSMLIELPTAQOANDYGPQOKSSSSKFSKSCIVAITTGLIRNVLISVLYWMIL 60

61 CCSKSKSTCSHCPCEIILWTRNGSCYFFSMKKDWMNSLKFCDKSGSHLLTFPDNGVK 120

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Db      61 CGSNVSTCASCPCSPCDRMWKYGNHCYFVSVEKQWNSLSLFCRLARDSHLVTITNQEMS 120
QY      121 LFGVYLGDFFWYIGLRNIDGMRWEGPALSL-RILTNLSLQCCGAIHRNGLOASSCEVAL 179
Db      121 LQVFLSEAFWCWGLRNNSGMRWEDGSPINFSRISNSFVQTCGAIKNKGLQASSCEVPL 180
QY      180 QWICKKY 186
Db      181 HGVCKKY 187

RESULT 5
US-10-416-384-1
; Sequence 1, Application US/10416384
; Publication No. US20050260244A1
; GENERAL INFORMATION:
; APPLICANT: University College London
; APPLICANT: GILLESPIE, STEPHEN
; TITLE OF INVENTION: Vaccine Component
; FILE REFERENCE: 068804-0000001
; CURRENT APPLICATION NUMBER: US/10/416,384
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04985
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: G30027433.2
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Plasmodium yoelii
US-10-416-384-1

Query Match      5.4%; Score 56; DB 6; Length 189;
Best Local Similarity 27.5%; Pred. No. 39;
Matches 19; Conservative 9; Mismatches 35; Indels 6; Gaps 2;

QY      10 LELPE-APQVQDESRRKALKAYLHRRPLSRFANVALGLTVILMSLMTQRIICGSKYST 68
Db      30 LELPQIVPQWMEVWRLEFVPHNPDAFMTASNAQSDFLVYVNGLAFYRAWLALGVEDS- 88
QY      69 GSHCPSCP1 77
Db      89 ----QACPL 93

RESULT 6
US-10-842-206-40
; Sequence 40, Application US/10842206
; Publication No. US20050256039A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, Jeffrey D
; APPLICANT: Sciore, Paul J
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: Cura 570A
; CURRENT APPLICATION NUMBER: US/10/842,206
; CURRENT FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 40
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-842-206-40

Query Match      4.1%; Score 42; DB 6; Length 188;
Best Local Similarity 28.4%; Pred. No. 12e+03;
Matches 19; Conservative 8; Mismatches 28; Indels 12; Gaps 4;

QY      107 GSHLTFPPDN--QGVR----LFG--EYLGQDFWYIGLRNIDGMRWEG----GPALSLRL 154
```

```
Db      51 GFHLQILPDGVSQGTRODHSLFGILEFISVAVLGVSIRGVDSGLYLGMNDKGELYGSEKL 110
QY      155 TNSLIQR 161
Db      111 TSECIFF 117

RESULT 7
US-10-980-459-32
; Sequence 32, Application US/10980459
; Publication No. US20050256042A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: ChillaKuru, Rajeev A.
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Larocheille, William J.
; APPLICANT: Lichenstein, Henri
; APPLICANT: Nandev, Pradyumna Kumar
; APPLICANT: Valax, Pascal
; APPLICANT: Yim, Zachary
; APPLICANT: Hahne, William
; TITLE OF INVENTION: Methods of Preventing and Treating Alimentary Mucositis
; FILE REFERENCE: Cura-57 AM
; CURRENT APPLICATION NUMBER: US/10/980,459
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: 10/435,087
; PRIOR FILING DATE: 2003-5-9
; PRIOR APPLICATION NUMBER: 10/842,179
; PRIOR FILING DATE: 2004-5-10
; PRIOR APPLICATION NUMBER: 60/541,728
; PRIOR FILING DATE: 2004-2-4
; PRIOR APPLICATION NUMBER: 60/545,278
; PRIOR FILING DATE: 2004-2-18
; PRIOR APPLICATION NUMBER: 60/____
; PRIOR FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 32
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-459-32

Query Match      4.1%; Score 42; DB 6; Length 188;
Best Local Similarity 28.4%; Pred. No. 1.2e+03;
Matches 19; Conservative 8; Mismatches 28; Indels 12; Gaps 4;

QY      107 GSHLTFPPDN--QGVR----LFG--EYLGQDFWYIGLRNIDGMRWEG----GPALSLRL 154
Db      51 GFHLQILPDGVSQGTRODHSLFGILEFISVAVLGVSIRGVDSGLYLGMNDKGELYGSEKL 110
QY      155 TNSLIQR 161
Db      111 TSECIFF 117

RESULT 8
US-10-945-853-2
; Sequence 2, Application US/10945853
; Publication No. US20050255117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Santocia-Nadel, Michele
; APPLICANT: Adkins, Heather
; APPLICANT: Miklasz, Steven Donald
; APPLICANT: Rayhorn, Paul
; APPLICANT: Schiffer, Susan Gail
; TITLE OF INVENTION: Cripco-Specific Antibodies
; FILE REFERENCE: BGNALL7CPPCN
; CURRENT APPLICATION NUMBER: US/10/945,853
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: PCT/US02/31462
```

```

? PRIOR FILING DATE: 2002-10-01
? PRIOR APPLICATION NUMBER: PCT/US02/11950
? PRIOR FILING DATE: 2002-04-17
? PRIOR APPLICATION NUMBER: 60/286,782
? PRIOR FILING DATE: 2001-04-26
? PRIOR APPLICATION NUMBER: 60/293,020
? PRIOR FILING DATE: 2001-05-17
? PRIOR APPLICATION NUMBER: 60/301,091
? PRIOR FILING DATE: 2001-06-26
? PRIOR APPLICATION NUMBER: 60/367,002
? PRIOR FILING DATE: 2002-03-22
? NUMBER OF SEQ ID NOS: 9
? SEQ ID NO 2
? LENGTH: 188
? TYPE: prt
? ORGANISM: Homo sapiens
US-10-945-853-2

```

	Query Match	4.0%	Score 41.5	DB 6	Length 188;
	Best Local Similarity	25.0%;	Pred. No. 1.4e+03;		
	Matches	18; Conservative	9; Mismatches	30;	Indels 15; Gaps 4
Oy	19 ODESRWKLKAVLHRPHLSRFAMVALGLTVILMSLLMWORI--LCGSGNDSTC---SHCP	73			
Dd	47 RDDSIWPEOEPAIRRSSQ-----RVLEPMGIQSKEINRTCC-LNGGTCLMSEFCA	96			
Oy	74 SCPIILTRNNGSH	85			
Dd	97 CPDSFYGRNCCH	108			

```

RESULT 9
US-10-467-657-2750
; Sequence 2750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 2750
; LENGTH: 188
; TYPE: prt
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2750

```

```

Query Match          3.9%; Score 40.5; DB 6; Length 188;
Best Local Similarity 24.6%; Pred. No. 1.8e+03;
Matches      15; Conservative    11; Mismatches   22; Indels   13; Gaps    4

QY      131 YVIGLRINDGMRWEG-GRPLSLRLINLSLRCRGALHNRGLQASCEVALQ--WICKYL 187
       :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      78 WWLYPFA---NWHGGGQTLMK-----TWKIGLCDLNGIOPSLHLRLRFIWACIFIV 127
       :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      188 Y 188
       :
Db      128 F 128

RESULT 10
US-10-131-826A-240
/ Sequence 240, Application US/10131826A
/ Publication No. US20050245730A1
/ GENERAL INFORMATION:

```

```

APPLICANT: Baker, Kevin F.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 240
LENGTH: 189
TYPE: prt
ORGANISM: Homo Sapien
US-10-131-826A-240

```

[illegible]

```
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 246
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-246
```

```
Query Match          3.9%; Score 40.5; DB 6; Length 189;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 5; Mismatches 16; Indels 9; Gaps 2;
```

```
QY 113 PPDNGVKLFGHYLGQDFWIG-----LRNIDGWRMEGG 146
Db 98 YPTN---NILNDIFGARLWPSBTVAIGLEKLDGKTEYGG 134
```

```
RESULT 12
US-10-467-657-2690
/ Sequence 2690, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 2690
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2690
```

```
Query Match          3.9%; Score 40.5; DB 6; Length 189;
Best Local Similarity 25.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 5; Mismatches 16; Indels 9; Gaps 2;
```

```
QY 113 PPDNGVKLFGHYLGQDFWIG-----LRNIDGWRMEGG 146
Db 98 YPTN---NILNDIFGARLWPSBTVAIGLEKLDGKTEYGG 134
```

```
RESULT 13
US-10-945-853-1
/ Sequence 1, Application US/10945853
/ Publication No. US20050255117A1
/ GENERAL INFORMATION:
/ APPLICANT: Biogen, Inc.
/ APPLICANT: Sanicola-Nadel, Michele
/ APPLICANT: Adkins, Heather
/ APPLICANT: Miklasz, Steven Donald
/ APPLICANT: Rayhorn, Paul
/ APPLICANT: Schiffer, Susan Gail
/ APPLICANT: Williams, Kevin
/ TITLE OF INVENTION: Crip-to-Specific Antibodies
```

```
/ FILE REFERENCE: BGNAL17CPCCN
/ CURRENT APPLICATION NUMBER: US/10/945, 853
/ CURRENT FILING DATE: 2004-09-20
/ PRIOR APPLICATION NUMBER: PCT/US02/31462
/ PRIOR FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: PCT/US02/11950
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: 60/286,782
/ PRIOR FILING DATE: 2001-04-26
/ PRIOR APPLICATION NUMBER: 60/293,020
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/301,091
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 60/367,002
/ PRIOR FILING DATE: 2002-03-22
/ NUMBER OF SEQ ID NOS: 9
/ SEQ ID NO 1
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-945-853-1
```

```
Query Match          3.6%; Score 37.5; DB 6; Length 188;
Best Local Similarity 24.7%; Pred. No. 3.7e+03;
Matches 18; Conservative 10; Mismatches 28; Indels 17; Gaps 5;
```

```
QY 19 QDESRLKAVLHRRPHLSRFAMVALGLTVMISLMTYQRIL---CCGSKDSTC---SHC 72
Db 47 RDSIWQEPSPAIRRSQ-RVPMG-----IQSKRLNRCC-LNGTCMLSGFC 95
```

```
QY 73 PSCPLWTRNGSH 85
Db 96 ACPSFYGRNCEH 108
```

```
RESULT 14
US-10-821-234-1393
/ Sequence 1393, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crahn, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 1393
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1393
```

```
Query Match          3.6%; Score 37; DB 6; Length 188;
Best Local Similarity 20.0%; Pred. No. 4.2e+03;
Matches 11; Conservative 11; Mismatches 15; Indels 18; Gaps 1;
```

```
QY 16 PVOVESRKLKAVLHRRP-----LSRFAMVALGLTVMIS 52
Db 24 PDRDISKNNRNVSNLLYQTNVLVAAMMISTVGLSPFNMILGGLVVLVTF 78
```

```
RESULT 15
US-10-528-031-4
/ Sequence 4, Application US/10528031
/ Publication No. US20050262577A1
/ GENERAL INFORMATION:
/ APPLICANT: ORIDIS BIOMED Forschungs- und Entwicklungs GmbH
```


Chrysomelidae

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 15:16:01 ; Search time 18.3009 Seconds
(without alignments)
988.409 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036
Sequence: 1 MADNSYSTLELPAPRVQD.....GLHASSCEVALQWICEKVL 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1164

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	I59421 mast cell function
2	65	6.3	188	2	C86508 hypothetrical prote
3	65	6.3	188	2	H72114 transcritpion regu
4	59.5	5.7	188	2	T33623 hypothetrical prote
5	56.5	5.5	189	2	B95865 conserved hypothet
6	56	5.4	189	2	AH1128 acetyltransferase
7	56	5.4	189	2	AC1489 acetyltransferase
8	55.5	5.4	189	2	A95110 acetyltransferase
9	55	5.3	189	2	E96569 probable IAA6 prot
10	55	5.3	189	2	S58493 auxin-induced prot
11	53.5	5.2	189	2	G97978 conserved hypothet
12	53.5	5.2	189	2	D81564 hypothetrical prote
13	53	5.1	189	2	T19559 hypothetrical prote
14	52	5.0	188	2	AC1355 methylphosphoriles
15	51.5	5.0	188	2	S74560 hypothetrical prote
16	49	4.7	188	2	I51347 MHC class I - Acta
17	49	4.7	189	2	B71542 hypothetrical prote
18	48.5	4.7	189	2	AH1029 probable membrane
19	48	4.6	188	2	G87336 conserved hypothet
20	48	4.6	189	2	S34632 dnat protein homol
21	47.5	4.6	188	2	TC4680 vascular endotheli
22	47.5	4.6	189	1	IVBO11 interferon alpha-1
23	47.5	4.6	189	1	IVBO11 interferon alpha-1
24	47.5	4.6	189	2	B72234 RNA polymerase sig
25	47.5	4.6	189	2	A25556 hypothetrical 21.2K
26	47	4.5	189	2	B29795 circumsporozoit p
27	47	4.5	189	2	A90172 conserved hypothet
28	46	4.4	188	2	A34014 integrin alpha-3 c
29	46	4.4	189	2	T02792 hypothetrical prote

30	45.5	4.4	188	2	A39787 teratocarcinoma-de
31	45.5	4.4	189	1	IWMSA6 interferon alpha-I
32	45.5	4.4	189	2	I49773 murine interferon
33	45.5	4.4	189	2	S52803 hypothetrical prote
34	45	4.3	188	2	S09789 hypothetrical prote
35	45	4.3	188	2	C69173 conserved hypothet
36	45	4.3	188	2	B83786 hypothetrical prote
37	44.5	4.3	189	1	IVBO1C interferon alpha-I
38	44.5	4.3	189	2	E64527 hypothetrical prote
39	44	4.2	188	1	UQ0534 coat protein Ken
40	44	4.2	189	2	T39519 probable signal se
41	44	4.2	189	2	F70125 conserved hypothet
42	44	4.2	189	2	T27306 hypothetrical prote
43	44	4.2	189	2	T02821 probable membrane
44	44	4.2	189	2	AG1947 hypothetrical prote
45	44	4.2	189	2	AB3586 probable transcrip

ALIGNMENTS

RESULT 1
I59421
mast cell function associated antigen - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59421
R:Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A>Title: A secretion inhibitory signal transduction molecule on mast cells is another C
A:Reference number: I59421; MUID:96016176; PMID:7568140
A:Accession: I59421
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-188 <RES>
A:Cross-references: UNIPROT:Q64335; UNIPARC:UPI0000030101; EMBL:X79812; NID:G1020141; P
C:Genetics:
A:Gene: mafa

Query Match 100.0%; Score 1036; DB 2; Length 188;
Best local Similarity 100.0%; Pred. No. 9.3e-90;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSYSTLELPAPRVQDSDRWKAVLHRCVSYLVWVALGLTVILMSLTYORTL 60
DB 1 MADNSYSTLELPAPRVQDSDRWKAVLHRCVSYLVWVALGLTVILMSLTYORTL 60

QY 61 CGSGKGFMCSCSRCPNLMWRNGSHCYFSMEKRDNSSLKFCADKSHLTFPDNQGVN 120
DB 61 CGSGKGFMCSCSRCPNLMWRNGSHCYFSMEKRDNSSLKFCADKSHLTFPDNQGVN 120

QY 121 LFOEYVGDPEFYWIGLRDIDGWRWEDPALSLTISNSVYQKGTTHRCGLHASSCEVALQ 180
DB 121 LFOEYVGDPEFYWIGLRDIDGWRWEDPALSLTISNSVYQKGTTHRCGLHASSCEVALQ 180

QY 181 WICEKVL 188
DB 181 WICEKVL 188

RESULT 2
C86508
hypothetical protein y99E (imported) - Chlamydomonas reinhardtii (strain J138)
C:Species: Chlamydomonas reinhardtii
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86508
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A>Title: Comparison of whole genome sequences of Chlamydomonas reinhardtii J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: C86508
A>Status: preliminary
A:Molecule type: DNA

A;Residues: 1-188 <STO>
A;Cross-references: UNIPROT:Q9Z944; UNIPARC:UPI00000D4127; GB:BA000008; NID:98978512; P
A;Experimental source: strain J138
C;Genetics:
A;Gene: yggE
;Superfamily: hypothetical protein HI0304

Query Match	6.3%	Score 65;	DB 2;	Length 188;
Best Local Similarity	33.8%	Pred. No. 82;		
Matches	22;	Conservative	6;	Mismatches 33;
			Indels	4;
			Gaps	3;

[illegible]

QY	116	NQGVN	120
		:	
Db	184	NLLLN	188

RESULT 3

```
transcription regulator, probable CP0633 [imported] - Chlamydomonadales (strains
C.Species: Chlamydomonadales pneumoniae, Chlamydomonadales pneumoniae
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
```

R. Kalkman, S. J. Mitchell, W. J. Marache, R. J. Lammel, C. J. Fan, J. J. Olinger, L. J. Grimwood, J. Nature Genet. 21, 385-389, 1999

Accession	Gene	Protein	Accession	Gene	Protein
A1	Accession: H72114		CD 150000000	MTF1	
A2	Molecule type: DNA		CD 150000000	MTF1	
A3	Residues: 1-188 <MAN>		CD 150000000	MTF1	

A: Experimental source: strain CW029
R: Read, T.D.; Brumham, R.C.; Shen, C.; Gall, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwalt, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
S.

A:Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: E81555

A.Residues: 1st188 <REA>
A.Cross-references: UNIPARC:UPI0000004127, GB:AE002221, GB:AE002161, NID:g7189543, PIDN
A.Experimental source: strain AR39, HL cells

A:Gene: yjgE; CP0633
C:Superfamily: hypothetical protein HI0304

Best Local Similarity	33.8%;	Pred. No. 82;							
Matches	22;	Conservative	6;	Mismatches	33;	Indels	4;	Gaps	3

Db 124 LCPFGSGWQAGGLEKEFELSNDFIARGNKDYFYSPEDLMALVLRKLGKRYASLSITVPD 183

Db 184 NLLN 188

RESULT 4
T33623
hypothetical protein F40G9.10 - *Caenorhabditis elegans*

C:\Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:\Accession: T33623
R:\Graves, T.; Sultterer, C.; Ozersky, P.

A:Description: The sequence of C. elegans cosmid F40G9
A:Reference number: Z21378
A:Accession: J33623

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-188 <GRA>
A:Cross-references: UNIPROT:Q9TZ75; UNIPARC:UPI00007BD20; EMBL:AF093919; PIDN:AAC68804.
A:Experimental source: strain Bristol N2, clone F4G59
C:Genetics:

A;Map position: 3
A;Introns: 63/3; 99/1; 113/3; 153/3

Best Local Similarity	24.7%	Pred. No. 2.7e+02	Matches	22	Conservative	12	Mismatches	30	Indels	25	Gaps	5
-----------------------	-------	-------------------	---------	----	--------------	----	------------	----	--------	----	------	---

```
Db      54 WFSYTNFCYKSTARANFNDAHNAACRSEGSGLASIHSLTENQFLVQLSAAGNRVNASKTNY 113
```

Db 114 V-----MIGLIFENRE--WSWTDGSSVN 134

RESULT 5

C.Species: Sinorhizobium meliloti
C.Date: 24-Aug-2001 #sequence 24-Aug-2001 #text_change 09-Jul-2004
CAccession: B95865

Chen Y., Pham-Duc T., Chai D., Vothofer E.T.: Hormones and nodulation factors as determinants of host plant specificity in legume root nodule symbiosis.

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A.Titile: The complete sequence of the 1.683-kb *PSYB* megaplasmid from the N2-fixing endodermis
 A.Reference number: A95842; NCID:2136508; PMID:11481431

A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-189 <R>

C.CID: 107600000CBP446 CB.P1E51995 RTDN.CAC6A5E6 1

A: Experimental source: strain 1021, megaplasmid pSYM
R: Galberth, F.; Finan, T.M.; Long, S.R.; Puller, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dranco, S.; Federspiel, N.A.; Fisher, R.F.

Science 293, 668-672, 2001
A. Authors: Kahn, D.; Kahn, M. L.; Kalman, S.; Keating, D. H.; Kiss, E.; Komp, C.; Lelaure, J.; Lebeault, P.; Vorholter, F. T.; Weidner, S.; Wells, D. H.; Wong, K.; Yeh, K.; Vandenbol, M.; Vorholter, F. T.; Weidner, S.; Wells, D. H.; Wong, K.; Yeh, K.

A:Reference number: A96039; MWID:21368234; PMID:11474104
 B:Contents: annotation
 C:Genetics: 2010c
 D:Year: 2010c

A;Genome:	plasmid
Query Match	
Score 56.5;	DB 2; length 189;
E 0.7%	Dseq NFE 1e-02

Matches 31; Conservative 15; Mismatches 54; Indels 43; Gaps 6

34 C V S T I L M V A L G L I Y I I M S L L L Y G R T L C C G S K G F M C S Q C S R C P I L M M R N G S H C Y Y F S M E K 93

Db 28 CASNPPTVIRIGSQT-----HNHACG-----CTK-----WRREGALFAQIAVAG 67

Qy 94 RDWNSLTK-----FCADKSGSHLLTFPDNGVNLFEQYVGEDFYWICL 135

Db 68 RD-NVAVTSGAEKLTQVDDPSAIIQRACRCDCGTHMY----GRIENTKPIFYGLDFVHTTEL 122

QY 136 RDIDGRWEDGPALSLITLSNSV 158

Db 123 SDEtGWSPPPEFAFVSIIESGV 145

AD1128
acetyltransferase homolog lmo0431 [imported] - *Listeria monocytogenes* (strain EGD-e)
C;Species: *Listeria monocytogenes*

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C/Accession: AH1128
 R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehli, H.; Jones, L.M.; Kretz, U.
 Science 294, 849-852, 2001
 A/Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A./Title: Comparative genomics of *Listeria species*.
 A/Reference number: AB1077; MUID:21537279; PMID:1167669
 A/Accession: AH1128
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-189 <GLA>
 A/Cross-references: UNIPROT:Q9Y9T9; UNIPARC:UPI0000054ESC; GB:NC_003210; PIDN:CAC98510.1
 A/Experimental source: strain EGD-e
 C/Genetics:
 A/Gene: lmo0431
 C/Superfamily: galactoside acetyltransferase

Query Match 5.4%; Score 56; DB 2; Length 189;
 Best Local Similarity 31.5%; Pred. No. 5.7e+02;
 Matches 28; Conservative 8; Mismatches 33; Indels 20; Gaps 5;

QY 99 SLKFCADKGSHTLPDPNQGVLFOEYVGEDFYWIGLRIDGKRWED---GPAISLIL 154
 DB 68 SLPEYSDFGKH-ITFGKNIFINLVTFV-----DLGGITIEDNVLIQPGALVTV 116

QY 155 SNSVQKCGTIRHCGH-ASSCEVALQWI 182
 DB 117 NHLVSPK---KRRGLRVAPICVKKNAMI 141

RESULT 7
 AC1489
 acetyltransferase homolog lin0451 [imported] - *Listeria innocua* (strain Clp11262)
 C/Species: *Listeria innocua*
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C/Accession: AC1489
 R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehli, H.; Jones, L.M.; Kretz, U.
 Science 294, 849-852, 2001
 A/Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tixeret, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A./Title: Comparative genomics of *Listeria species*.
 A/Reference number: AB1077; MUID:21537279; PMID:1167669
 A/Accession: AC1489
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-189 <GLA>
 A/Cross-references: UNIPROT:Q92EK8; UNIPARC:UPI000000CC232; GB:AL592022; PIDN:CAC95603.1
 A/Experimental source: strain Clp11262
 C/Genetics:
 A/Gene: lin0451
 C/Superfamily: galactoside acetyltransferase

Query Match 5.4%; Score 56; DB 2; Length 189;
 Best Local Similarity 31.5%; Pred. No. 5.7e+02;
 Matches 28; Conservative 8; Mismatches 33; Indels 20; Gaps 5;

QY 99 SLKFCADKGSHTLPDPNQGVLFOEYVGEDFYWIGLRIDGKRWED---GPAISLIL 154
 DB 68 SLPEYSDFGKH-ITFGKNIFINLVTFV-----DLGGITIEDNVLIQPGALVTV 116

QY 155 SNSVQKCGTIRHCGH-ASSCEVALQWI 182
 DB 117 NHLVSPK---KRRGLRVAPICVKKNAMI 141

RESULT 8
 A95110
 acetyltransferase, GNAT family [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C/Species: *Streptococcus pneumoniae*
 C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 31-Dec-2004
 C/Accession: A95110
 R/Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heik on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple, neon, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A./Title: Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*.
 A/Reference number: A95000; MUID:21357209; PMID:11463916
 A/Accession: A95110
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-189 <KUR>
 A/Cross-references: UNIPROT:Q97876; UNIPARC:UPI0000051661; GB:AE005672; PIDN:AAK75074.1
 A/Experimental source: strain TIGR4
 C/Genetics:
 A/Gene: SP0953
 C/Superfamily: ribosomal protein serine N-acetyltransferase

Query Match 5.4%; Score 55.5; DB 2; Length 189;
 Best Local Similarity 24.0%; Pred. No. 6.4e+02;
 Matches 23; Conservative 14; Mismatches 36; Indels 23; Gaps 4;

QY 95 DNSSLKFCADKGSHTLPDPNQGVLFOEYVGEDFYWIGLRIDGKRWEDGPA 149
 DB 28 DDAEAFDASDKGNRTYFPPTQSLERKNIAQPYLANPL-----GRW----- 71

QY 150 SLILSNSVQKCGTIRHCGH-ASSCEVALQWICEK 185
 DB 72 GIEIKSNG--QITGITDHLKIDSVLKAAGIYINK 105

RESULT 9
 E96569
 probable IAA6 protein, 42631-41742 [imported] - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: E96569
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marshall Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: E96569
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-189 <STO>
 A/Cross-references: UNIPROT:Q38824; UNIPARC:UPI0000126696; GB:AE005173; NID:G6862944; P
 A/Experimental source: strain TIGR4
 C/Genetics:
 A/Gene: P14G24.10
 A/Map position: 1
 C/Superfamily: auxin-induced protein aux28

Query Match 5.3%; Score 55; DB 2; Length 189;
 Best Local Similarity 25.2%; Pred. No. 7.1e+02;
 Matches 28; Conservative 16; Mismatches 43; Indels 24; Gaps 5;

QY 3 DNGISTLELPAPRODDSRMKYKAVLRPCVSYL-----VMVALGLITVILMSLL 55
 DB 52 ENSVSVSEVDESLPVV-----KSQAVGMPVPSYRKKNNEBASAIAGVVKV-SMDGVP 104

QY 56 YORTLCCGSKGFMCSQCRCPNLM-----MENGSHCYT---FSMEKRW 96
 DB 105 YMRKIDGSSNSYINLVTVLENTFGCIGIGVAKGKKCEYIIITYEDKRD 155

[illegible]

C:Accession: D81564
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of *Chlamydia trachomatis* Mohn and *Chlamydia pneumoniae* AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: D81564
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-189 <REA>
 A:Cross-references: UNIPROT:Q9K250; UNIPARC:UP100000CCCTB; GB:AE002214; GB:AE002161; NID
 C:Superfamily: Chlamydia pneumoniae hypothetical protein Cpn0218
 A:Gene: CP0547
 Query Match
 Best Local Similarity 33.3%; Score 53.5; DB 2; Length 189;
 Matches 22; Conservative 10; Mismatches 21; Indels 13; Gaps 4;
 QY 13 PAPPVQDDSRMKV-KAVLHRCVSYLVWY-----ALGLITVILMSLLYQRTLCGSK 65
 DB 110 PIHPDMMKRYREVLQAVTEILGLVILVFDIIGCFIAFLVAILSLLY-----CNST 164
 QY 66 GPMCSQ 71
 DB 165 -FTCVQ 169
 RESULT 13
 T19559
 hypothetical protein C29F3.4 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T19559
 R:Matthews, L.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19142
 A:Accession: T19559
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-189 <M1L>
 A:Cross-references: UNIPROT:O17613; UNIPARC:UP100000783D6; EMBL:Z81043; PIDD: CAB02800.1;
 C:Experimental source: clone C29F3
 C:Genetics:
 A:Gene: CESP:C29F3.4
 A:Map position: 5
 A:Introns: 32/3; 133/3
 Query Match
 Best Local Similarity 18.1%; Score 53; DB 2; Length 189;
 Matches 28; Conservative 17; Mismatches 54; Indels 56; Gaps 6;
 QY 75 CPNLMMR---NGSHCYTFSMEKRDWNSLKFC-ADKGSHL----- 110
 DB 35 CPAGWFOFORATGLWCYIFATPGAGWTPQAACQANGANINGFESAERTQFIRKLKE 94
 QY 111 -----LTFPDNOCVNLFOEY-----VGEDFWIG-----LRDIDGWR 142
 DB 95 PCSNYSKPEEDMLASLAPYTFPHIGAMRCAPCTVNDPFWLVNGVSNNDNTPANDYDSL 154
 QY 143 WEDGALSLSLIS---NSVYQKCGTIHRCGLHAS 173
 DB 155 DLTGDCLSMDLGNNGQYNDITCDAAETAYSCGKPA 189
 RESULT 14
 AC1355
 methylphosphotriester-mono alkyltransferase and transcription regulator homolog lmo2243 [



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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:14:56 ; Search time 96.4956 Seconds
(without alignment)
1374.564 Million cell updates/sec

Title: US-09-811-367b-5

Perfect score: 1036
Sequence: 1 MADNSTYSTLELPAAPRVOD.....GLHASSCEVALQWICEKILP 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 9256

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1036	100.0	188	2	Q64335_RAT
2	838	80.9	188	2	O88713_MOUSE
3	545.5	52.7	189	2	O75613_HUMAN
4	525.5	50.7	189	2	O43198_HUMAN
5	164.5	15.9	188	2	O62Y73_CHICK
6	164.5	15.9	188	2	O62Y76_CHICK
7	159.5	15.4	188	1	CLC51_HUMAN
8	159.5	15.4	188	2	O52M11_HUMAN
9	134	12.9	189	2	O61969_MOUSE
10	121	11.7	189	2	O8C614_MOUSE
11	92.5	8.9	188	2	O9W012_DROME
12	87	8.4	189	2	O96D19_HUMAN
13	85.5	8.3	189	2	O60S03_CAEHR
14	75.5	7.3	188	2	O9W3D8_DROME
15	73	7.0	189	2	O18202_CAEEL
16	69	6.7	188	2	O84R12_ARATH
17	66.5	6.4	188	2	O4UHL7_TREAN
18	65	6.3	188	1	Y139_CHLPP
19	62.5	6.0	188	2	O7Q249_ANOGA
20	61.5	5.9	188	2	O7K7K8_CAEEL
21	60.5	5.8	189	2	O86L29_MYTEO
22	60	5.8	188	2	O9DVM3_SHIV1
23	59.5	5.7	188	2	O4IE26_GIBZE
24	59.5	5.7	188	2	O9TZ75_CAEEL
25	59	5.6	188	2	O8Q3K3_SHIV1
26	58.5	5.5	188	2	O68P15_CENSC
27	57	5.5	189	2	O5L5N9_CHLAB
28	56.5	5.5	188	2	O9HFA9_9HETE
29	56.5	5.5	189	1	GFA_RHIME
30	56	5.4	189	2	O723NO_LISMF
31	56	5.4	189	2	O8Y9T9_LISMO

32	56	5.4	189	2	O92EK8_LISIN	O92EK8 listeria in
33	55.5	5.4	188	2	O5D9G7_SCHJA	O5D9G7 schistosoma
34	55.5	5.4	189	2	O97R76_STRPN	O97R76 streptococc
35	55	5.3	189	1	IAA6_ARATH	O38824 arabidopsis
36	55	5.3	189	2	O8A4F4_BACTN	O8A4F4 bacteroides
37	54.5	5.3	189	2	O7OR55_SHIV1	O7OR55 human immun
38	54.5	5.3	189	2	O7ZH46_SHIV1	O7ZH46 human immun
39	54.5	5.3	189	2	O7ZH59_SHIV1	O822P9 chlamydophi
40	54	5.2	189	1	Y630_CHLCP	O751J3 dictyosteli
41	54	5.2	189	2	O75JD3_DICDI	O41Y05 corynebacte
42	54	5.2	189	2	O41Y05_CORUK	O61XP3 human immun
43	54	5.2	189	2	O61XP3_SHIV1	O8dB05 vibrio vuln
44	53.5	5.2	188	2	O8DB05_VIBVU	O9K250 chlamydia p
45	53.5	5.2	189	2	O9K250_CHLPP	

ALIGNMENTS

RESULT 1
Q64335_RAT PRELIMINARY; PRT; 188 AA.
ID Q64335_RAT
AC Q64335;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE MAFPA protein (Mast cell function associated antigen).
GN Name=Klrg1; Synonyms=MAFA, mafa;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague Dawley; TISSUE=Testis;
RX MEDLINE=97240766; PubMed=9120279;
RT Bocsk J P., Gutmann M D., Pecht I.;
RT "Analysis of the gene encoding the mast cell function-associated
RT antigen and its alternatively spliced transcripts.";
RT J. Immunol. 158:3235-3243(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96016176; PubMed=7568140;
RA Gutmann M.D., Tal M., Pecht I.;
RT "A secretory inhibitory signal transduction molecule on mast cells is
RT another C-type lectin.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).
DR EMBL; X97191; CAA65829.1; -; Genomic_DNA.
DR EMBL; X79812; CAA65208.1; -; mRNA.
DR EMBL; X79192; CAA65829.1; JOINED; Genomic_DNA.
DR EMBL; X97193; CAA65829.1; JOINED; Genomic_DNA.
DR EMBL; X97194; CAA65829.1; JOINED; Genomic_DNA.
DR EMBL; X97195; CAA65829.1; JOINED; Genomic_DNA.
DR PIR; I59421; I59421.
DR HSSP; P26718; IKCG.
DR Ensemble; ENSRNOG0000014918; Rattus norvegicus.
DR RSD; 61978; Klrg1.
DR GO; GO:0005529; F: sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C-TYPE_HECTIN_2; 1.
SQ SEQUENCE 188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;
Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 2; Ie-92;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MADNSTYSTLELPAAPRVODSRMKVAVLHRCVSYLVNVALGLFTVIMSLLYORTL 60
Db 1 MADNSTYSTLELPAAPRVODSRMKVAVLHRCVSYLVNVALGLFTVIMSLLYORTL 60

QY 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPDNGVN 120
DB 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPDNGVN 120
QY 121 LFGYVGEDEFWYIGLRIDGWRWEDGDPALSLSTLSNSVYQCGTTHRCGLHASSCEVALQ 180
DB 121 LFGYVGEDEFWYIGLRIDGWRWEDGDPALSLSTLSNSVYQCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVL 188
DB 181 WICEKVL 188

RESULT 2

088713_MOUSE PRELIMINARY; PRT; 188 AA.

ID 088713_MOUSE PRELIMINARY; PRT; 188 AA.
AC 088713_MOUSE PRELIMINARY; PRT; 188 AA.
DT 01-NOV-1998 (TRMBLrel. 08, Created)
DT 01-NOV-1998 (TRMBLrel. 11, Last sequence update)
DT 10-MAY-2005 (TRMBLrel. 30, Last annotation update)
DE Mast cell function-associated antigen 2F1 (killer cell lectin-like receptor G1) (MAFA).
GN Name=KIRG1; Synonyms=Mafa, mafa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C.B-17 SCID;
RA Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT "2F1 antigen, the mouse homolog of the rat 'mast cell function-associated antigen', is a lectin-like type II transmembrane receptor expressed by natural killer cells."
RT Eur. J. Immunol. 28:4409-4417(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;
RA Voehringer D., Kaufmann M., Pitcher H.;
RT "Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KIRG1), the mouse homologue of MAFA."
RT Immunogenetics 52:206-211(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=99077501; PubMed=9862665;
RA Blaier C., Kaufmann M., Pitcher H.;
RT "Virus-activated CD8 T cells and lymphokine-activated NK cells express the mast cell function-associated antigen MAFA, an inhibitory C-type lectin."
RT J. Immunol. 161:6451-6454(1998).
RL EMBL; AF097357; AAD03718.1; -; mRNA.
DR EMBL; AF317727; AAK4082.1; -; Genomic DNA.
DR EMBL; AJ010751; CA09342.1; -; mRNA.
DR HSSP; Q13241; 1B6E.
DR Ensemble; ENSMUSG0000030114; Mus musculus.
DR MGI; MGI:1355294; KIRG1.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005529; F:sugar binding; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLCCT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR Lectin; Receptor.
FT CHAIN 2 188
FT SEQUENCE 188 AA, 21396 MW, 876336802E1134F1 CRC64;
Query Match 80.9%; Score 838; DB 2; Length 188;

Best Local Similarity 80.7%; Pred. No. 3.6e-73;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSIYSTELEPAAPRYQDDSRWKVAVLRPCVSYLWVALGILTYILMSLLYQRTL 60
DB 1 MADNSIYSTELEPAAPRYQDDSRWKVAVLRPCVSYLWVALGILTYILMSLLYQRTL 60
QY 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPDNGVN 120
DB 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPDNGVN 120
QY 121 LFGYVGEDEFWYIGLRIDGWRWEDGDPALSLSTLSNSVYQCGTTHRCGLHASSCEVALQ 180
DB 121 LFGYVGEDEFWYIGLRIDGWRWEDGDPALSLSTLSNSVYQCGTTHRCGLHASSCEVALQ 180
QY 181 WICEKVL 187
DB 181 WICEKVL 187

RESULT 3

075613_HUMAN PRELIMINARY; PRT; 189 AA.

ID 075613_HUMAN PRELIMINARY; PRT; 189 AA.
AC 075613_HUMAN PRELIMINARY; PRT; 189 AA.
DT 01-NOV-1998 (TRMBLrel. 08, Created)
DT 01-NOV-1998 (TRMBLrel. 08, Last sequence update)
DT 01-FEB-2005 (TRMBLrel. 29, Last annotation update)
DE ITIM-containing receptor MAFA-L (Mast cell function-associated antigen homolog).
GN Name=MAFA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=99057052; PubMed=9842918;
RA Butcher S., Arney K.L., Cook G.P.;
RT "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene complex and expressed by basophils and NK cells."
RT Eur. J. Immunol. 28:3755-3762(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=99077194; PubMed=9862378;
RA Hanke T., Corral L., Vance R.E., Raulat D.H.;
RT "2F1 antigen, the mouse homolog of the rat 'mast cell function-associated antigen', is a lectin-like type II transmembrane receptor expressed by natural killer cells."
RT Eur. J. Immunol. 28:4409-4417(1998).
RL EMBL; AF081675; AAC32200.1; -; mRNA.
DR EMBL; AF097358; AAD03719.1; -; mRNA.
DR HSSP; Q13241; 1B6E.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLCCT; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR Lectin; Receptor.
FT CHAIN 2 189 AA, 21206 MW, FA9023F1523656A8 CRC64;
FT SEQUENCE 189 AA, 21206 MW, FA9023F1523656A8 CRC64;

Query Match 52.7%; Score 545.5; DB 2; Length 189;
Best Local Similarity 55.1%; Pred. No. 9.3e-45;
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTELEPAAPRYQDDSRWKVAVLRPCVSYLWVALGILTYILMSLLYQRTL 60
DB 1 MTDVITYMLELPRTAQNDNYGPOQKSSSRPSCCVATALGLTVALLSVLLYQWIL 60
QY 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPDNGVN 120
DB 61 CCGSKGFMCSCQSRCPNLMMRNGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPDNGVN 120

Dd		61	CQGSNSTRSCACSPCPDRMKRYGNHCCYFVSVEKDMNSLFECLARDSHLLVITDNGMS	120
Oy		121	LFOEYVEDPYWIGLRIDIDGRMEDGPAISLS-ILSNVYOKCTTHRCGLHASCEVAL	179
Dd		121	LLAQFLSEAPFCMIGIRNNSGRMWEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL	180
Oy		180	QMICEKV 186	
Dd		181	HWCCKV 187	
 RESULT 4				
ID	O43198_HUMAN	PRELIMINARY;	PRT;	189 AA.
AC	O43198;			
DT	01-JUN-1998	(TREMBLrel. 06, Created)		
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Maat cell function-associated antigen.			
GN	Name=MAFA,			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	Tissue=enzyme digested lung;			
RX	MEDLINE=96438735; PubMed=9765598; DOI=10.1016/S0167-4781(98)00107-9;			
RA	Lamers M.B., Lamont A.G., Williams D.H.;			
RL	Biochim. Biophys. Acta 1399:209-212(1998).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	Tissue=enzyme digested lung;			
RA	Lamers M.B.A.C., Lamont A.G., Williams D.H.;			
RL	Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF034952; AAC34731.1; -; mRNA.			
DR	HSSP; Q13241; 1B6E.			
DR	GO; GO:0016021; C:integral to membrane; TAS.			
DR	GO; GO:0004872; F:receptor activity; TAS.			
DR	GO; GO:0005529; F:sugar binding; TAS.			
DR	GO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.			
DR	GO; GO:0006968; P:cellular defense response; TAS.			
DR	GO; GO:0006954; P:inflammatory response; TAS.			
DR	InterPro; IPR01304; Lectin_C.			
DR	Pfam; PF00059; lectin_C; 1.			
DR	SMART; SM00034; CLECT_1.			
DR	PROSITE; PS50041; C_TYPE_LECTIN_2; 1.			
SQ	SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;			
 Query Match 50.7%; Score 525.5; DB 2; Length 189;				
Best Local Similarity 53.5%; Pred. No. 8, le=43;				
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 14				
Oy	1 MDNSIYSTLEDPAPBRVDDSRMWKAVLAHPCVSYLVMAVLGIITYILNSLIYYRTL	60		
Dd	1 MNDSVIYNLDELPTAQONDYGPQQSKSSSRKPCSLVAIRTLGLITVALSLVLYQWIL	60		
Oy	61 CGGSKCFMCSQCSRPNLMNRGSHCYYSMEKRPMNSLTFRCADKGSHLLTFPDNOGVN	120		
Dd	61 CGGSNSTASCPSCPDRMMKKYGNHCYYPSVEKDMNSLFECLARDSHLLVITDNGMS	120		
Oy	121 LFOEYVEDPYWIGLRIDIDGRMEDGPAISLS-ILSNVYOKCTTHRCGLHASCEVAL	179		
Dd	121 LLQVFLSEAPFCMIGIRNNSGRMWEDGSPINFSRISNSFVOTCGAINKNGLOASSCEVPL	180		
Oy	180 QMICEKV 186			
Dd	181 HWCCKV 187			
 RESULT 5				

ID	Q6ZYP3_CHICK	Q6ZYP3_CHICK PRELIMINARY;	PRT;	188 AA.
AC	Q6ZYP3;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	B-1ec proteain.			
OS	Name=B-1ec;			
OC	Gallus gallus (chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxId=9031;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Bursa;			
RX	PubMed=15749883;			
RA	Rogers S.L., Gobel T.W., Viertelboeck B.C., Milne S., Beck S.,			
RT	Kaufman J.,			
RT	"Characterisation of C-type lectin-like receptors B-NK and B-1ec			
RT	reveals that the NK Complex and the MHC share a common ancestral			
RL	region."			
RL	J. Immunol. 174:3475-3483(2005).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Bursa;			
RA	Rogers S.L.;			
RT	"Characterisation of C-type lectin-like receptors in the chicken			
RT	MHC."			
RT	Thesis (2002), Department of Pathology and Microbiology, University of			
RL	Bristol, Bristol, United Kingdom.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Bursa;			
RA	Kaufman J.F.;			
RL	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; A1634337; CAG25421.1; -, mRNA.			
DR	HSPF; Q9H8P0; 1K9J.			
DR	GO; GO:0005529; F:sugar binding; IEA.			
DR	InterPro; IPR002353; AntiFreezeI1.			
DR	InterPro; IPR001304; Lectin_C.			
DR	Pfam; PF00059; Lectin_C_1.-			
DR	PRINTS; PR00356; ANTIFREEZEI1.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.			
DR	PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.			
SO	SEQUENCE 188 AA; 21053 MW; 6AD5AC3C9B8BF440 CRC64;			
Query Match	15.9%;	Score 164.5;	DB 2;	Length 188;
Best Local Similarity	25.0%;	Pred. No. 9.4e-08;		
Matches	40;	Conservative 33;	Mismatches 68;	Indels 19; Gaps 77
QY	34 CYSYLVWVALGLITVILMSLLYQRTLCCKSGKGFV--CSQCSRCPENLWMRNGSHCYFSM 91			
DB	26 CVPFQPLTMA-AVFYVLTLITNAVF-----AVQAFQPHNQPCACQCFWIDIGRKCYYFSB 78			
QY	92 EKRDWSSLIKFCADKQSHLLTFPPDNGVNLFOEYVGEDFYIIGLADIG----WRNEGCP 147			
DB	79 DESNWTSSQNNCSALGASIAVFDASLEDLSFTMRHKSSPHWVGL-SREGKHPEWVNRS 137			
QY	148 ALS--LSLISNSVOKCGTIHRCGLHAASCEVALQWICK 185			
DB	138 PLSHLFOVQDGL---CAVLGADGLSSHCSTRRWVCTK 174			
RESULT 6				
AC	Q6ZYP6_CHICK		PRT;	188 AA.
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	B-1ec protein.			

```

GN Name=B-1ec;
OS Gallus gallus (Chicken).
OC Archosauria; Neozoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=bone marrow;
RX PubMed=15749883;
RA Rogers S.L., Gobel T.W., Vierterboeck B.C., Milne S., Beck S.,
RA Kauffman J.;
RT "Characterisation of C-type lectin-like receptors B-NK and B-1ec
RT reveals that the NK Complex and the MHC share a common ancestral
RT region.";
RL J. Immunol. 174:3475-3483 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=bone marrow;
RA Rogers S.L.;
RT "Characterisation of C-type lectin-like receptors in the chicken
RT MHC.";
RL Theiss (2002), Department of Pathology and Microbiology, University of
RL Bristol, Bristol, United Kingdom.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Tissue=bone marrow;
RA Kauffman J.F.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ634334; CAG25418.1; -; mRNA.
DR HSP; O9H8F0; 1K9J.
DR GO; GO:0005529; F.sugar binding; IEA.
DR InterPro; IPR002353; Antifreeze1.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN_1.
DR PROSITE; PS50041; C TYPE LECTIN 2; 1.
SO SEQUENCE 188 AA; 20957 MW; 3FDBD9B9F9E41 CRC64;

Query Match 15.9%; Score 164.5; DB 2; Length 188;
Best Local Similarity 24.5%; Pred. No. 9.4e-08;
Matches 39; Conservative 32; Mismatches 71; Indels 17; Gaps 6;

QY 34 CYSYLVMAVAGLITVIMSLYLQRTLCGSGKFM--CSQSCRCPMLMNRNSHCYPSM 91
DB 26 CVTFOITMA-AVFTVILLITAVAF-----AVQAFQHPQCAQCPDWIGFRGKCYFSE 78
QY 92 EKRDNNSLKPCADKSHLTFPPDNGVNLFOEYVGEDFYWIGLR---DIDGRMEDGPA 148
DB 79 DESNNTSSGNNSALGASLAVDSADLSFTYRHKSSPHWVGLSREGHEHMEVNRSP 138

QY 149 IS--LSIISNVVQKGTIRGCLHASSCEVALQWICEK 185
DB 139 LSHLFOVQGDGL---CAVLGDAGLSSSHCSARRNWCTK 174

RESULT 7
CICSA HUMAN STANDARD; PRT; 188 AA.
ID 09NY25; 09UK00;
AC 09NY25; 09UK00;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE C-type lectin domain family 5 member A (C-type lectin superfamily
DE member 5) (Myeloid DAP12-associating lectin) (MDL-1).
GN Name=CICSA; Synonyms=CLECSF5, MDL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxId=9606;

```

```

RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2), FUNCTION, TISSUE SPECIFICITY,
RP INTERACTION WITH TYROBP, AND MUTAGENESIS OF LYS-16.
RX MEDLINE=99380598; PubMed=10449773; DOI=10.1073/pnas.96.17.9792;
RA Baker A.B.H., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;
RT "Myeloid DAP12-associating lectin (MDL)-1 is a cell surface receptor
RT involved in the activation of myeloid cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).
RA Mueller A., Merz H., Feller A.C.;
RT "Expression of MDL-1 in human blood and cell lines.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Mace J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vandbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozerov P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strommatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Moesener J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Speith J.,
RA Bieri T.A., Nelson J.O., Berkowitz N., Wohlmann P.E., Cook L.L.,
RA Hickmottlam M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen B.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Sims E., Levy R., Clendenning J., Kaul R., Kent W.J., Frey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164 (2003).
RN [4]
RP FUNCTION: May be involved in proinflammatory activation of myeloid
RP cells via TYROBP-mediated signaling in a calcium-dependent manner.
CC [1] SUBUNIT: Interacts with TYROBP.
CC [2] TISSUE SPECIFICITY: Expressed in peripheral blood monocytes and in
CC the monocyte/macrophage cell lines U937 and MonoMac6, but not in
CC cell lines of other origins. Expression is down-regulated when
CC monocytes differentiate into dendritic cells.
CC [3] SIMILARITY: Contains 1 C-type lectin domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AF139768; AAF02491.1; -; mRNA.
CC EMBL; AJ271684; CAB71334.1; -; mRNA.
CC EMBL; AC073647; AAS07444.1; -; genomic DNA.
CC HSP; P22897; IEHG.
CC Ensembl; ENSG00000090269; Homo sapiens.
CC HGNC; HGNC:2054; CLECSF5.
CC MIM; 604987; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005488; F:binding; TAS.
CC GO; GO:0006988; P:cellular defense response; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR002353; Antifreeze1.

```


DR Interpro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C; 1.
 DR Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP NUCLEOTIDE SEQUENCE.
 RP TISSUE=lung and heart;
 RG NIH MGC Project;
 RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC093714; AAH93714.1; -; mRNA.
 KW Lectin.
 SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;
 Query Match 15.4%; Score 159.5; DB 1; Length 188;
 Best Local Similarity 25.5%; Pred. No. 2.9e-07;
 Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;
 QY 40 MWALGILTYIL---MSLL-----YQRTLCGS-----XGFMCS 70
 DB 5 MTSGLIVVLLKVVGMFLFLYPQIFNKNDGFTTTSYGVQIFGSSSPSPNGFIT 64
 QY 71 QC--SRCPNLMNRNGSHCYFMSKRDWNSLKFCADKGSLLTTPDNGVNLFOEYV 128
 DB 65 RSYGVCPDMEFYQARCFPLSTSSSWNSRDFCKGKSTLAVTPEKLFLODITDA 124
 QY 129 DRYWIGL---RDIDGRWEDGALSLISLSNVQKCGTHRCGL---HASSCEVALQW 181
 DB 125 EKYFGLIYHREKRWKRWINSVFNQVNTQNFNCATI---GLTKTFDAASCDISYR 181
 QY 182 ICEK 185
 DB 182 ICEK 185
 RESULT 8
 ID Q52M11 HUMAN PRELIMINARY; PRT; 188 AA.
 AC Q52M11;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE C-type lectin, superfamily member 5.
 GN Name=CLC5A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=lung and heart;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grose L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datschenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP NUCLEOTIDE SEQUENCE.
 RP TISSUE=lung and heart;
 RG NIH MGC Project;
 RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC093714; AAH93714.1; -; mRNA.
 KW Lectin.
 SQ SEQUENCE 188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;
 Query Match 15.4%; Score 159.5; DB 2; Length 188;
 Best Local Similarity 25.5%; Pred. No. 2.9e-07;
 Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;
 QY 40 MWALGILTYIL---MSLL-----YQRTLCGS-----XGFMCS 70
 DB 5 MTSGLIVVLLKVVGMFLFLYPQIFNKNDGFTTTSYGVQIFGSSSPSPNGFIT 64
 QY 71 QC--SRCPNLMNRNGSHCYFMSKRDWNSLKFCADKGSLLTTPDNGVNLFOEYV 128
 DB 65 RSYGVCPDMEFYQARCFPLSTSSSWNSRDFCKGKSTLAVTPEKLFLODITDA 124
 QY 129 DRYWIGL---RDIDGRWEDGALSLISLSNVQKCGTHRCGL---HASSCEVALQW 181
 DB 125 EKYFGLIYHREKRWKRWINSVFNQVNTQNFNCATI---GLTKTFDAASCDISYR 181
 QY 182 ICEK 185
 DB 182 ICEK 185
 RESULT 9
 ID Q61969 MOUSE PRELIMINARY; PRT; 189 AA.
 AC Q61969;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Natural killer cell receptor-PI (Fragment).
 GN Name=NKR-PI 34;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murine; Mus.
 NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=BALB/c;
 RX MEDLINE=9238663; PubMed=1517565;
 RA Giorda R., Weisberg E.P., Ip T.K., Trucco M.;
 RT "Genomic structure and strain-specific expression of the natural
 RT killer cell receptor NKR-PI."
 RL J. Immunol. 149:1957-1963 (1992).
 DR EMBL; X64719; CAA45972.1; -; mRNA.
 DR HSSP; 007108; 1FMS.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR Interpro; IPR001304; Lectin_C.
 DR Pfam; PF00059; Lectin_C; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.
 KW Receptor.
 FT NON_TER 1 1

FT NON TER 189 189
 SQ SEQUENCE 189 AA; 21310 MW; D605E4BD967073B0 CRC64;
 Query Match 12.9%; Score 134; DB 2; Length 189;
 Best Local Similarity 23.4%; Pred. No. 8.7e-05;
 Matches 41; Conservative 29; Mismatches 73; Indels 32; Gaps 8;
 Oy 16 PRVODS-----RWKVAVALHPCVSY-----LVMVALGLTLVIMSLTLORTLCCG- 63
 16 PLSLPTCCCPW-----HRLAKRGCGALLIVYVIGLCVIVSLVSKSSVQKICADV 69
 Db 64 ---SKGFWCSCCSCRCPLMNMNGSHCYVFSMEKDWNSLRFKADKSHLLTFPDNGCV 119
 70 QENRHTTTCGVNLECPQDWLISHRDSCFRVFPQVSNTEWEGQADCGKKGATLLIDQBEL 129
 Oy 120 NLFQEVGDEFL--YWTGLR-----DIDGRWEDGPPALSLSLNSVQK---CGTI 165
 130 RFLDSIKERKYNKSPWIGLFTPLDMN-WRMINGTTFNSDVLKITGTENGSCATTI 183
 Db
 RESULT 10
 Q8C634 MOUSE
 ID Q8C634_MOUSE PRELIMINARY; PRT; 189 AA.
 AC Q8C634;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 library, clone:492502D21 product:hypothetical C-type lectin domain
 containing protein, full insert sequence (Similar to C lectin-related
 protein A).
 DE Name:492502D21RLK;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217651; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaasikawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
 RA Brownstein W.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehama J., Mazzarelli J., Mombaerts P.,
 RA Norone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru R., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanapin A., Matsuda H., Batilov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbin L.E., Cousins S.,
 RA Dalla E., Dregan T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Goidik A., Gough J.,
 RA Gustimond S., Gustinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kani A., Kawai H., Kawasawa Y., Kedzierzki R.M., King B.L.,
 RA Kanagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Serou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszewski A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
 RA Sun N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RL [7]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abotil J.F., Agayanni A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernack B.P., Bhandari D., Bolintiner S.,
 RA Borkova D., Botchan M.R., Bouck Y., Brokstein P., Brottaker S.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Chesney S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paoliis R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes K., Duggan-Rocha S., Durkin B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foerster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodet A., Gong F., Gorelli J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.U., Mei M.-H., Ibbegan C.,
 RA Jaitani M., Kalish P., Kapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lai Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlehnha N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reneker K., Remington K., Saunders R.D.C., Scheel F., Shen H.,
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Gibbs R.A., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Ceilinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Wuzny D.M., Nelson C.R.,
 RA Pacle J.M., Pak S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Ceilinker S.E.,
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.S., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Ceilinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;

QY 178 ALQWICE 184
DB 178 LRFVQ 184

RESULT 14
ID Q9W3D8 DROME PRELIMINARY; PRT; 188 AA.
AC Q9W3D8;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG12111-PA (At17652p).
GN ORFNames=CG12111;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
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RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abri1 J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Baillet R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadiu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foutel C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glied A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ijzerman C.,
RA Jalali M., Kalish F., Karpen G.H., Ke Z., Kesterson J.A., Ketchum K.A.,
RA Jallat B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlehnina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
[2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=2242605; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacled J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettecourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacled J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[6]
RN NUCLEOTIDE SEQUENCE.
RG FlyBase;
RA Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
[7]
RN NUCLEOTIDE SEQUENCE.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guatin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo C.J., Pacled J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003444; AAP46391.1; -; Genomic_DNA.
DR EMBL; AY070795; AAL48417.1; -; mRNA.
DR HSSP; P35247; 1B08.
DR Ensembl; CG12111; Drosophila melanogaster.
DR FlyBase; FBgn0030050; CG12111.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C TYPE LECTIN 2; 1.
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Best Local Similarity 20.6%; Pred. No. 42;
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DB 48 FVRIGDNYTYIIFPMKNKNVQQAAGACRMMAHLASIEDKEMELAIKYMAKGFKNNDYF 107
QY 132 WIGLRDI--DG---WR-----WEDGPALSLSLNSVYQKCTTH---RCGLHA 172
DB 108 WISGNDIGTGEGARYWNSNGRPMTYAPW--NGPKQMPDNYGN--ENC--VHMFATREMIND 162
QY 173 SSGCEVALQWICENKLP 188
DB 163 ANCKIQMLVYCEATEP 178

RESULT 15
018202_CAEEL

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DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
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GN ORFNames=Y48E1B.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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OX NCBI_TaxID=6239;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN= Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
   investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z93393; CAB07697.2; -; Genomic_DNA.
DR PIR; T27020; T27020.
DR HSSP; P22030; 1FVU.
DR Ensembl; Y48E1B.9; Caenorhabditis elegans.
DR WormBase; WBGene0013008; Y48E1B.9.
DR WormPep; Y48E1B.9; CE36239.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR01104; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR Complete proteome; Hypothetical protein.
SQ SEQUENCE 189 AA; 21548 MW; 192DA964586072F0 CRC64;

Query Match 7.0%; Score 73; DB 2; Length 189;
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DB 82 YLFFERKSWDNAERHRCGFGAHLAI-DNEAKNGFVTLINSETSPAWIGMK 135
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Search completed: January 9, 2006, 15:35:29
Job time : 98.4956 secs

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OM protein - protein search, using SW model

Run on: January 9, 2006, 15:25:12 ; Search time 25.2885 Seconds
(without alignments)
614.628 Million cell updates/sec

Title: US-09-811-367b-5
Perfect score: 1036
Sequence: 1 MADNSYSTLELPAPRVQD.....GHASSCEVALQWICKVLP 188

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 991

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5.COMB.pep.*
2: /cgn2_6/prodata/1/1aa/6.COMB.pep.*
3: /cgn2_6/prodata/1/1aa/H.COMB.pep.*
4: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep.*
5: /cgn2_6/prodata/1/1aa/RS.COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1036	100.0	188	2	US-08-722-126A-5
2	1036	100.0	188	4	PCT-US95-04258-5
3	54	5.2	189	2	US-09-270-767-31816
4	54	5.2	189	2	US-09-270-767-47033
5	53.5	5.2	189	2	US-09-198-452A-1169
6	50.5	4.9	188	2	US-09-438-185A-761
7	50	4.8	188	2	US-09-270-767-42805
8	47.5	4.6	188	1	US-08-469-427A-5
9	47.5	4.6	188	1	US-08-609-443B-5
10	47.5	4.6	188	1	US-08-569-063C-5
11	47.5	4.6	188	2	US-08-851-896-5
12	47.5	4.6	188	2	US-09-252-991A-29925
13	47.5	4.6	188	2	US-09-107-433-5087
14	47.5	4.6	189	2	US-09-198-452A-135
15	47	4.5	188	2	US-09-543-681A-7232
16	45.5	4.4	188	1	US-07-749-001-5
17	45.5	4.4	188	1	US-08-154-198-5
18	45.5	4.4	188	1	US-08-463-135-5
19	45.5	4.4	188	1	US-08-464-023A-5
20	45.5	4.4	189	2	US-09-902-540-14285
21	44.5	4.3	189	2	US-09-482-273-107
22	44	4.2	188	2	US-09-134-000C-6806
23	44	4.2	188	2	US-09-248-796A-18895
24	44	4.2	189	2	US-09-270-767-35760
25	44	4.2	189	2	US-09-270-767-50997
26	43.5	4.2	188	2	US-09-270-767-58978
27	43.5	4.2	188	2	US-09-605-703B-1580

28	43	4.2	188	2	US-09-134-000C-3652	Sequence 3652, Ap
29	42.5	4.1	188	2	US-09-393-627B-19	Sequence 19, Appl
30	42.5	4.1	188	2	US-09-438-185A-957	Sequence 957, App
31	42.5	4.1	189	2	US-09-902-540-10384	Sequence 10384, A
32	42	4.1	188	2	US-09-122-443-14	Sequence 14, Appl
33	42	4.1	188	2	US-09-558-089-14	Sequence 14, Appl
34	42	4.1	188	2	US-09-558-087-14	Sequence 14, Appl
35	42	4.1	188	2	US-09-248-796A-20257	Sequence 20257, A
36	42	4.1	188	2	US-09-558-474-14	Sequence 14, Appl
37	42	4.1	189	2	US-09-489-038A-11286	Sequence 11286, A
38	42	4.1	189	2	US-09-248-796A-20999	Sequence 20999, A
39	41.5	4.0	188	1	US-08-142-449B-14	Sequence 14, Appl
40	41.5	4.0	189	1	US-08-026-758-1	Sequence 1, Appl1
41	41.5	4.0	189	2	US-09-487-792-7	Sequence 7, Appl1
42	41.5	4.0	189	2	US-09-908-594-7	Sequence 7, Appl1
43	41	4.0	188	1	US-08-469-427A-11	Sequence 11, Appl
44	41	4.0	188	1	US-08-609-443B-11	Sequence 11, Appl
45	41	4.0	188	1	US-08-569-063C-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-722-126A-5
Sequence 5, Application US/08722126A
Patent No. 6034227
GENERAL INFORMATION:
APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: UNITED STATES OF AMERICA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT=1A
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-722-126A-5
Query Match 100.0%; Score 1036; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 4,8e-105;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADNSYSTLELPAAPRVODDSRMKVKAVLHRCVSYLWVALGLTITVIMSLLYORTL 60
DB 1 MADNSYSTLELPAAPRVODDSRMKVKAVLHRCVSYLWVALGLTITVIMSLLYORTL 60

QY 61 CCGSKGFMCSQCSRCPNLMRMNGSHCYF5MEKRDWNSLKFCAKGSHTLTFPNOGVN 120
DB 61 CCGSKGFMCSQCSRCPNLMRMNGSHCYF5MEKRDWNSLKFCAKGSHTLTFPNOGVN 120

QY 121 LFOEYVGEDFWYIGLRDIDGMRWEDGPAISLSISNSVYVCKGTIHRGGLHASSCEVALQ 180
DB 121 LFOEYVGEDFWYIGLRDIDGMRWEDGPAISLSISNSVYVCKGTIHRGGLHASSCEVALQ 180

QY 181 WICEKVLTP 188
DB 181 WICEKVLTP 188

RESULT 2
PCT-US95-04258-5
; Sequence 5, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04258
; FILING DATE: 06-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109257
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: PCHT=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04258-5

Query Match 100.0%; Score 1036; DB 4; Length 188;
Best Local Similarity 100.0%; Pred. No. 4.8e-105;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 LFOEYVGEDFWYIGLRDIDGMRWEDGPAISLSISNSVYVCKGTIHRGGLHASSCEVALQ 180
DB 121 LFOEYVGEDFWYIGLRDIDGMRWEDGPAISLSISNSVYVCKGTIHRGGLHASSCEVALQ 180

QY 181 WICEKVLTP 188
DB 181 WICEKVLTP 188

RESULT 3
US-09-270-767-31816
; Sequence 31816, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31816
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-31816

Query Match 5.2%; Score 54; DB 2; Length 189;
Best Local Similarity 21.2%; Pred. No. 6.8e+02;
Matches 18; Conservative 10; Mismatches 31; Indels 26; Gaps 3;

QY 22 SRWK-----VKAVLHRCVSYLWVALGLTITVIMSLLY-----Q 57
DB 102 SKMKNLQPLDQIKDYFGAKVALYFAW--LGFYTMILPISVGVLCFLYGTITWNSDPIS 159

QY 58 RTLCCSGKFMCSQCSRCPNLMRN 82
DB 160 RDICDDNGTINCPQCDRSCDYWRLN 184

RESULT 4
US-09-270-767-47033
; Sequence 47033, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47033
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47033

Query Match 5.2%; Score 54; DB 2; Length 189;
Best Local Similarity 21.2%; Pred. No. 6.8e+02;
Matches 18; Conservative 10; Mismatches 31; Indels 26; Gaps 3;

QY 22 SRWK-----VKAVLHRCVSYLWVALGLTITVIMSLLY-----Q 57
DB 102 SKMKNLQPLDQIKDYFGAKVALYFAW--LGFYTMILPISVGVLCFLYGTITWNSDPIS 159

QY 58 RTLCCSGKFMCSQCSRCPNLMRN 82
DB 160 RDICDDNGTINCPQCDRSCDYWRLN 184

RESULT 5
US-09-198-452A-1169


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; Sequence 1169, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifflaie, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1169
; LENGTH: 189
; TYPE: PRF
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1169

Query Match
Best Local Similarity 33.3%; Pred. No. 7.7e+02;
Matches 22; Conservative 10; Mismatches 21; Indels 13; Gaps 4;

QY 13 PAAPRQDDSRMRY-KAVLHRCVSYLVWV-----ALGLITVILMSLLYQRTLCGSGK 65
DB 110 P1HPRDKMYRFEVLDAVIEIIGLVILVFDIIGCFPLAVAILSLLY-----CNST 164
QY 66 GFMCSSQ 71
DB 165 -FTCVQ 169

RESULT 6
US-09-438-185A-761
; Sequence 761, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 761
; LENGTH: 188
; TYPE: PRF
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0759
US-09-438-185A-761

Query Match
Best Local Similarity 27.6%; Pred. No. 1.6e+03;
Matches 21; Conservative 9; Mismatches 21; Indels 25; Gaps 4;
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; Sequence 42805, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42805
; LENGTH: 188
; TYPE: PRF
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42805

Query Match
Best Local Similarity 21.3%; Pred. No. 1.8e+03;
Matches 33; Conservative 16; Mismatches 48; Indels 58; Gaps 7;

QY 17 RVQDD-----SRWKVAVLHRCVSYLVWVAGLTVI-INSLLYQRTLCGSGKGFNC 69
DB 27 RKQDDKQDDTEGRMRKLLCVAVCTTNGQLVXDIXFIPKLSFLXY--FPGIXPRAPRC 84
QY 70 SQCSRCPNLMNRNCHCYFSMEKRDWNSLRFCA-----DKGSHLTPPDQGVNLPQE 124
DB 85 S-----FSINLNVW-----KVCATLTKRKXKILMKAPKSNWSVSQISE 122
QY 125 YGDEPFYWGIGLDIDGWRWEDGPALSLTISNSV 159
DB 123 -----PKLSASVCAITVV 135

RESULT 8
US-08-469-427A-5
; Sequence 5, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Alitalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979cp2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 5:
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SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-5

Query Match      4.6%; Score 47.5; DB 1; Length 188;
Best Local Similarity 41.7%; Pred. No. 3.5e+03;
Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1

QY      149 LSLSILNSV---VOKCGTIRRCG 169
|||::|||::|||
Db       56 LSMELMGNVVXQLVPSCVTQVRGC 79

RESULT 9
US-08-609-443B-5
Sequence 5, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSSE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:

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US-08-609-443B-5      TISSUE TYPE: adult mouse heart
Query Match           4.6%; Score 47.5; DB 1; Length 188;
Best Local Similarity 41.7%; Pred. No. 3.5e+03;
Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

Oy      149 LSLSLNSV---VOKGTHRCG 169
      ||::||::||::||::||::||
Db      56 LSMELMGNVVKKQIVPSCVTYVRCG 79

RESULT 10
US-08-569-063C-5
; Sequence 5, Application US/08569063C
; Patent No. 582839
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAULISOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-569-063C-5

Query Match           4.6%; Score 47.5; DB 1; Length 188;
Best Local Similarity 41.7%; Pred. No. 3.5e+03;
Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1;

Oy      149 LSLSLNSV---VOKGTHRCG 169
      ||::||::||::||::||::||
Db      56 LSMELMGNVVKKQIVPSCVTYVRCG 79

```

RESULT 11
US-08-851-896-5
Sequence 5, Application US/08851896
Patent No. 6331301
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,896
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-851-896-5
Query Match 4.6%; Score 47.5; DB 2; Length 188;
Best Local Similarity 41.7%; Pred. No. 3.5e+03;
Matches 10; Conservative 4; Mismatches 7; Indels 3; Gaps 1;
QY 149 LSLSLISNSV---VQKGTIHRG 169
DB 56 LSLMLGNVVKQVPSCTVQRCG 79
RESULT 12
US-09-252-991A-29925
Sequence 29925, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29925
LENGTH: 188
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29925
Query Match 4.6%; Score 47.5; DB 2; Length 188;
Best Local Similarity 20.5%; Pred. No. 3.5e+03;
Matches 24; Conservative 12; Mismatches 38; Indels 43; Gaps 4;
QY 81 RNSHCYFSEMEKRWNSLKEFC-----ADK---GSHLLTPDNQVNLFOEX 125
DB 96 RNASHVRLFQLSEDDSDQDIVFVGVGSDGVGPSADODSDNGMDPDPPTRTWFFRGY 155
QY 126 VQEDFYWIGLRIDGWRWEDGPAISLISNSVQKCGTIRHCGHAASCEVALQMI 182
DB 156 VSD-----PPDPRAANTLVATQATQNSG-----AGQMI 184
RESULT 13
US-09-107-433-5087
Sequence 5087, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5087:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES

ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...188
SEQUENCE DESCRIPTION: SEQ ID NO: 5087:
US-09-107-433-5087

Query Match 4.6%; Score 47.5; DB 2; Length 188;
Best Local Similarity 23.5%; Pred. No. 3.5e+03;
Matches 19; Conservative 13; Mismatches 26; Indels 23; Gaps 4;

QY 88 YFSMEKRDWNSL-----KFC-----ADKSHLTFPDNQ-----GVNLFQDY 125
DB 105 YF-LRKDAMSGFMTEVVRKICQLSFEERGLKQLSIITHLNEASQVALKSGFSLPRQF 163
QY 126 VGEDFYWIGLRDIDGMRWEDG 146
DB 164 KGSDDRYTRKMRDYLEFRYVKG 184

RESULT 14
US-09-198-452A-135
; Sequence 135, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffee, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 135
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-135

Query Match 4.6%; Score 47.5; DB 2; Length 189;
Best Local Similarity 22.2%; Pred. No. 3.5e+03;
Matches 22; Conservative 11; Mismatches 41; Indels 25; Gaps 5;

QY 64 SKGFMC-----QCSRCPN-----LMNRNGSHCYFSEMERD--WNSLKF---CA 104
DB 89 ANFYCKYFGLDAMSCENKFCPLPHEGKITFWLRE-----VOAEKKNTVTLSLSDCAE 142
QY 105 DKGSHLTFPDNQGVNLFQDYVGEDFYWIGLRDIDGMRW 143
DB 143 EDFCYLRRMELFGKLEKQADEHAYVWLAQDLDSHAM 181

RESULT 15
US-09-543-681A-7232
; Sequence 7232, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7232
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7232

Query Match 4.5%; Score 47; DB 2; Length 188;
Best Local Similarity 32.8%; Pred. No. 3.9e+03;
Matches 19; Conservative 4; Mismatches 29; Indels 6; Gaps 3;

QY 55 LYQRTLCGSGFMCSQCSCRCP---NLMMRNG--SHCY-FSMERKRDWNSLKFCAK 106
DB 118 LLQRKSRFGKIFVACNCPYPCQFVLANKPINGECYCHYPLMEKRSSQGVRLVCASK 175

Search completed: January 9, 2006, 15:38:01
Job time : 26.2885 secs


```

; APPLICANT: Takahashi, No. US20020155110A1uak1
; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAPA)
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-811-367B-3
```

```

Query Match      80.9%; Score 838; DB 3; Length 188;
Best Local Similarity 80.7%; Pred. No. 2.4e-76;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
```

```

QY      1  MADNSIYSTLELPAAPRVQDDSRMKYKAVLHRCVSYLVMAVALLITVILMSLLIYQRTL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1  MADSSIYSTLELPEAPQVQDESRMKLKAVALHRLHPSRFAMVALGLITVILMSLLMYQRL 60

QY      61  CCGSKGFMCSQCSRCPNLMNRGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPNOGVN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61  CCGSDSTCSHCPCSPDILMTNRGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPNOGVK 120

QY      121  LFOEYVGEDFYWIGLRIDIDGMRWEDGPAISLSILNSVQKCGTTHRCGLHASSCEVALQ 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121  LFEGLVGDQDFYWIGLRIDIDGMRWEGGPAISLILNLSLILQRCGALHRCGLQASSCEVALQ 180

QY      181  WICEKV 187
      |||:|||||
DB      181  WICKKVL 187

RESULT 3
US-10-207-655-196
; Sequence 196, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-196
```

```

Query Match      52.7%; Score 545.5; DB 4; Length 189;
Best Local Similarity 55.1%; Pred. No. 8.7e-47;
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;
```

```

QY      1  MADNSIYSTLELPAAPRVQDDSRMKYKAVLHRCVSYLVMAVALLITVILMSLLIYQRTL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1  MDSVIYSMLPLPTAQONDYGPQOKSSSRPSCCLVAIALGLITVILSVLILYQWL 60

QY      61  CCGSKGFMCSQCSRCPNLMNRGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPNOGVN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61  CCGSVSTCASCPCSPDMMKYGNHCYFYSVEKDWNSLSEFCIARDSHLITVITDQNS 120

QY      121  LFOEYVGEDFYWIGLRIDIDGMRWEDGPAISLSILNSVQKCGTTHRCGLHASSCEVAL 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121  LLQVFLSEAFWIGLRINNSGMRWEDGSPINFSRISNSFVQTCGAINKNGIQAASSCEVPL 180
```

```

QY      180  QWICEKV 186
      |||:|||||
DB      181  HMVCKKV 187
```

```

RESULT 4
US-10-756-149-5210
; Sequence 5210, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5210
```

```

; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5210
```

```

Query Match      52.7%; Score 545.5; DB 5; Length 189;
Best Local Similarity 55.1%; Pred. No. 8.7e-47;
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;
```

```

QY      1  MADNSIYSTLELPAAPRVQDDSRMKYKAVLHRCVSYLVMAVALLITVILMSLLIYQRTL 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1  MDSVIYSMLPLPTAQONDYGPQOKSSSRPSCCLVAIALGLITVILSVLILYQWL 60

QY      61  CCGSKGFMCSQCSRCPNLMNRGSHCYFYSMEKRDWNSLKFCDKGSHTLTFPNOGVN 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61  CCGSVSTCASCPCSPDMMKYGNHCYFYSVEKDWNSLSEFCIARDSHLITVITDQNS 120

QY      121  LFOEYVGEDFYWIGLRIDIDGMRWEDGPAISLSILNSVQKCGTTHRCGLHASSCEVAL 179
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      121  LLQVFLSEAFWIGLRINNSGMRWEDGSPINFSRISNSFVQTCGAINKNGIQAASSCEVPL 180

QY      180  QWICEKV 186
      |||:|||||
DB      181  HMVCKKV 187
```

```

RESULT 5
US-09-811-367B-1
; Sequence 1, Application US/09811367B
; Patent No. US20020155110A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: Takahashi, No. US20020155110A1uak1
```

```

; APPLICANT: Mikayama, Toshifumi
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAPA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09/811,367B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/190,716
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-367B-1
```

```

Query Match      50.7%; Score 525.5; DB 3; Length 189;
Best Local Similarity 53.5%; Pred. No. 9.1e-45;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
```

[illegible]

```

RESULT 6
US-09-759-130B-83
; Sequence 83, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kiret, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MP100-5350M1M
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-83

Query Match      15.4%; Score 159.5; DB 3; Length 188;
Best Local Similarity 25.5%; Pred. No. 8.6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;

```

[illegible]

```

RESULT 7
US-10-741-790-83
/ Sequence 83, Application US/10741790
/ Publication No. US20040121396A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: McCarthy, Sean A
/ APPLICANT: Fraser, Christopher C
/ APPLICANT: Sharp, John D
/ APPLICANT: Barnee, Thomas S
/ APPLICANT: Kirtz, Susan J
/ APPLICANT: Mackey, Charles R
/ APPLICANT: Myers, Paul S
/ APPLICANT: Leiby, Kevin R
/ APPLICANT: Wrighton, Nicolas
/ APPLICANT: Goodearl, Andrew
/ APPLICANT: Holtzman, Douglas A
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
/ TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
/ TITLE OF INVENTION: USES.
/ FILE REFERENCE: MP100-535OMNIM
/ CURRENT APPLICATION NUMBER: US/10/741,790
/ CURRENT FILING DATE: 2003-12-19
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 83
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-741-790-83

Query Match 15.4%; Score 159.5; DB 4; Length 188;
Best Local Similarity 25.5%; Pred. No. 8.6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7;

```

```

Db      5  MISSLIYVVLKVGWMTLEFLYFPQIFNKSNGFTTTSYGVQSQIFGSSSPSPNGFITTT
QY      71  QC--SRCENLWMRNSHCYFYSMEKRDWNSLTKPCADKGSHTLTPPDNGVNLFGEEYVGE
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65  RSYGVCPKDEMEFYQARCFPLSTSSSWNESRDFCKGKSTLAIYVNTPEKLFQDITDA
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      129  DFWYIGL---RDIDGWRDEGDPALSLSLISVVOKCGIHHCGL---HASSCEVALQW
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      125  EKYFGLIYHHEKKRWIINNSVFNGVNTNQNQNFNCATI---GLTKTFDAASCDISYR
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      182  ICEK 185
        |||
        182 ICEK 185
        |||
        182 ICEK 185

RESULT 8
US-10-287-436A-69
; Sequence 69, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-69

Query Match      15.4%; Score 159.5; DB 5; length 188;
Best Local Similarity 25.5%; Pred. No. 8,6e-08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7

QY      40  MVALGLITVIL---MSLLT-----YQRTLCCGS-----KGFMC 70
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      5  MISSLIYVVLKVGWMTLEFLYFPQIFNKSNGFTTTSYGVQSQIFGSSSPSPNGFITTT
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      71  QC--SRCENLWMRNSHCYFYSMEKRDWNSLTKPCADKGSHTLTPPDNGVNLFGEEYVGE
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65  RSYGVCPKDEMEFYQARCFPLSTSSSWNESRDFCKGKSTLAIYVNTPEKLFQDITDA
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      129  DFWYIGL---RDIDGWRDEGDPALSLSLISVVOKCGIHHCGL---HASSCEVALQW
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      125  EKYFGLIYHHEKKRWIINNSVFNGVNTNQNQNFNCATI---GLTKTFDAASCDISYR
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      182  ICEK 185
        |||
        182 ICEK 185
        |||
        182 ICEK 185

RESULT 9
US-10-287-436A-1251
; Sequence 1251, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1251

```

```
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-267-436A-1251
```

Query Match 15.4%; Score 159.5; DB 5; Length 188;
Best Local Similarity 25.5%; Pred. No. 8,6e+08;
Matches 47; Conservative 31; Mismatches 65; Indels 41; Gaps 7

OY 40 MWALGLTVIL-----MSILL-----YORTLCCGS-----KGPMCS 70
| : | : ||
DB 5 MISGIIIVLVKVMQMTFLLELPPIFNKSNDGFPTTSRYGVSGIIFGSSSPSNGFIYT 64
OY 71 QC--SRCNLMNRNSHCYYFSMEKRDNSSLKPCADRGSHLLTTPDQGVLFGVEYCE 128
| : | : ||
DB 65 RSYGVCPCKDWEFYGARCFPLSTBESSWNESRDPFCGKGSLTAIVNTDEKLFDIDIDA 124

OY 129 DFWVIGL---RDIDGRWEDGPALSLSITNSVVQCCTHIRCGL----HASSCEVALQM 181
|||:
DB 125 EKFTFGLHYHEBEKKRWNNINNVENGANTNONNCATICT---GLTKTFDAASCDISYRR 181

OY 182 ICEK 185
|||:
DB 182 ICEK 185

RESULT 10
US-09-764-870-487
Sequence 487, Application US/09764870
Patent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 487
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-870-487

Query Match 14.8%; Score 153.5; DB 3; Length 189;
Best Local Similarity 27.2%; Pred. No. 3,5e+07;
Matches 34; Conservative 25; Mismatches 61; Indels 5; Gaps 4

OY 64 SKGMFCGCC-SRCPNLMNRNSHCYYFSMEKRDNSSLKFCAKDGGSHLLTFPDNGCVNL 122
|||:
DB 65 SKG-CIRCECAPCEDMWLYGRKCIFYSEEBPDMWTGRQYCHTHEAVLAIVSQKELEFM 122

OY 123 QEYVGEDPYWIGLRDI-DGWEMEDGPALSLSITNSVVQCCTHIRCGLHASCEVALQM 181
|||:
DB 123 KFTFRRE-PWIGLRKVGEFEHWANGDDPPDTFTTAGEGECVFUEPTRLVSTECLMTRPW 181

OY 182 ICEKY 186
|||:
DB 182 VCSKM 186

RESULT 11
US-10-125-540-487
Sequence 487, Application US/10125540
Publication No. US20030059875A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ1AC1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm

APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
NUMBER OF SEQ ID NOS: 321
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 48
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-893-48

Query Match 7.3%; Score 75.5; DB 4; Length 189;
Best Local Similarity 34.9%; Pred. No. 26;
Matches 15; Conservative 7; Mismatches 20; Indels 1; Gaps 1;

OY 70 SOCSR-CPNLWRNSHCYFSPMEKRDWNSLKFCADKSHLL 111
DB 138 ANCSAPCFQDWMHGENCYLFSGSGSPNWEKSEQECLSLDAKLL 180

RESULT 15
US-10-424-599-250285
Sequence 250285, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 250285
LENGTH: 188
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_68035C.1.pep
US-10-424-599-250285

Query Match 6.1%; Score 63.5; DB 4; Length 188;
Best Local Similarity 24.5%; Pred. No. 4.3e+02;
Matches 26; Conservative 15; Mismatches 36; Indels 29; Gaps 6;

OY 79 WMRNSHCYFSPMEKRDWNS-----LKPCA---DKGSHLTFP-DNOGV----- 119
DB 86 WHVDGHHFYVGMDSGQSTSRSNYNLRDTSRCTGVQVPSKWTAVNPLDVGMMNVR 145
OY 120 --NLFOEYVGEDPFYIGLRDIDGMWEDGPALSLISNSVQKCG 163
DB 146 SENMAYRYLGQGFYLGVSFANSWRDE-----YPIPSNALP--CG 183

Search completed: January 9, 2006, 15:56:00
Job time : 73.5381 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 15:36:43 ; Search time 10.6478 Seconds
(without alignments)
149.966 Million cell updates/sec

Title: US-09-811-367b-5
Perfect score: 1036
Sequence: 1 MADNSIVSTLELPAAPRVQD.....GIHASSCEVALQWICEKVP 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues
Total number of hits satisfying chosen parameters: 97

Minimum DB seq length: 188
Maximum DB seq length: 189

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1036	100.0	188	US-10-055-877-206	Sequence 205, App
2	838	80.9	188	US-10-055-877-205	Sequence 206, App
3	545.5	52.7	189	US-10-055-877-207	Sequence 207, App
4	525.5	50.7	189	US-10-055-877-209	Sequence 209, App
5	45	4.3	189	US-10-467-657-246	Sequence 246, App
6	45	4.3	189	US-10-467-657-2690	Sequence 2690, App
7	44.5	4.1	188	US-10-131-826A-240	Sequence 240, App
8	42.5	4.0	188	US-10-945-853-2	Sequence 2, Appl1
9	41	4.0	189	US-11-064-774A-117	Sequence 117, App
10	41	4.0	189	US-11-137-465-60	Sequence 60, Appl
11	40	3.9	188	US-10-111-826A-232	Sequence 232, App
12	40	3.9	189	US-10-793-626-2976	Sequence 2976, App
13	40	3.9	189	US-10-793-626-2976	Sequence 3000, Appl
14	39.5	3.8	188	US-10-945-853-1	Sequence 1, Appl1
15	39.5	3.8	189	US-11-147-492-10	Sequence 10, Appl
16	39	3.8	189	US-11-147-492-12	Sequence 12, Appl
17	39	3.8	189	US-11-147-492-16	Sequence 16, Appl
18	38	3.7	188	US-10-821-234-1393	Sequence 1393, Ap
19	38	3.7	188	US-10-528-031-4	Sequence 4, Appl1
20	37.5	3.6	189	US-11-147-492-28	Sequence 28, Appl
21	37	3.6	189	US-11-147-492-10	Sequence 10, Appl
22	35	3.4	188	US-10-884-730-88	Sequence 88, Appl
23	35	3.4	189	US-10-467-657-4044	Sequence 4044, Ap
24	34.5	3.3	189	US-11-147-492-20	Sequence 20, Appl
25	34	3.3	189	US-11-147-492-26	Sequence 26, Appl

26	33.5	3.2	189	US-10-467-657-4524	Sequence 4524, Ap
27	33	3.2	189	US-10-995-551-643	Sequence 643, App
28	33	3.2	189	US-11-147-492-14	Sequence 14, Appl
29	32.5	3.1	188	US-11-036-797-37	Sequence 37, Appl
30	32.5	3.1	189	US-10-873-528-15	Sequence 15, Appl
31	32.5	3.1	189	US-10-147-492-6	Sequence 6, Appl1
32	32.5	3.1	189	US-11-147-492-18	Sequence 18, Appl
33	32.5	3.1	189	US-11-147-492-22	Sequence 22, Appl
34	32	3.1	188	US-10-980-388-101	Sequence 101, App
35	32	3.1	188	US-11-147-492-8	Sequence 8, Appl1
36	32	3.1	189	US-10-416-384-1	Sequence 1, Appl1
37	31.5	3.0	188	US-10-884-730-294	Sequence 294, App
38	31.5	3.0	188	US-10-884-730-322	Sequence 322, App
39	31.5	3.0	188	US-10-485-517-221	Sequence 221, App
40	31	3.0	188	US-10-842-206-40	Sequence 40, Appl
41	31	3.0	188	US-10-980-459-32	Sequence 32, Appl
42	30.5	2.9	189	US-11-147-492-24	Sequence 24, Appl
43	30.5	2.9	189	US-10-467-657-3184	Sequence 3184, Ap
44	30	2.9	188	US-10-467-657-4400	Sequence 4400, Ap
45	30	2.9	188	US-10-467-657-7132	Sequence 7132, Ap

ALIGNMENTS

RESULT 1
US-10-055-877-206
; Sequence 206, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Vellizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zernhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patuturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Boldog, Ferenc
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21400-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25

```
/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ PRIOR FILING DATE: 2001-03-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 206
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-10-055-877-206
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Query Match          100.0%; Score 1036; DB 6; Length 188;
Best Local Similarity 100.0%; Pred. No. 1.7e-104;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MADNSYSTLELPAAPRYODSRMKVKAVLHRCVSYLWVALGLTYILMSLLYORTL 60
DB 1 MADNSYSTLELPAAPRYODSRMKVKAVLHRCVSYLWVALGLTYILMSLLYORTL 60
QY 61 CCGSGKFMCSQCSRCPNLMRNKSGHCYFYSMEKRDWNSSLKFCADKSGHLLTFPNOGVN 120
DB 61 CCGSGKFMCSQCSRCPNLMRNKSGHCYFYSMEKRDWNSSLKFCADKSGHLLTFPNOGVN 120
QY 121 LFGYVGEDEFYWGIGRIDGWRWEDGPAISLISNSVYQKGTIHRGGLHASSCEVALQ 180
DB 121 LFGYVGEDEFYWGIGRIDGWRWEDGPAISLISNSVYQKGTIHRGGLHASSCEVALQ 180
QY 181 WICKKVL 188
DB 181 WICKKVL 188

RESULT 2
US-10-055-877-205
/ Sequence 205, Application US/10055877
/ Publication No. US20050288241A1
/ GENERAL INFORMATION:
/ APPLICANT: Decristofaro, Marc
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Miller, Charles
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Zhong, Mei
/ APPLICANT: Anderson, David
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Rattelli, Luca
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Zernhusen, Bryan
/ APPLICANT: Andrew, David
/ APPLICANT: Mezes, Peter
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Eissen, Andrew
/ APPLICANT: Wolenc, Adam
/ APPLICANT: Baumgartner, Jason
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Vernet, Corinne
/ APPLICANT: Taupier Jr., Raymond
/ APPLICANT: Pena, Carol
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Li, Li
/ APPLICANT: Casman, Stacie
```

```
/ APPLICANT: Boldog, Ference
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
/ FILE REFERENCE: 21402-251
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,598
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/263,799
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/264,117
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,139
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 205
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-055-877-205
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Query Match          80.9%; Score 838; DB 6; Length 188;
Best Local Similarity 80.7%; Pred. No. 3.2e-83;
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
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QY 1 MADNSYSTLELPAAPRYODSRMKVKAVLHRCVSYLWVALGLTYILMSLLYORTL 60
DB 1 MADNSYSTLELPAAPRYODSRMKVKAVLHRCVSYLWVALGLTYILMSLLYORTL 60
QY 61 CCGSGKFMCSQCSRCPNLMRNKSGHCYFYSMEKRDWNSSLKFCADKSGHLLTFPNOGVN 120
DB 61 CCGSGKFMCSQCSRCPNLMRNKSGHCYFYSMEKRDWNSSLKFCADKSGHLLTFPNOGVN 120
QY 121 LFGYVGEDEFYWGIGRIDGWRWEDGPAISLISNSVYQKGTIHRGGLHASSCEVALQ 180
DB 121 LFGYVGEDEFYWGIGRIDGWRWEDGPAISLISNSVYQKGTIHRGGLHASSCEVALQ 180
QY 181 WICKKVL 187
DB 181 WICKKVL 187

RESULT 3
US-10-055-877-207
/ Sequence 207, Application US/10055877
/ Publication No. US20050288241A1
/ GENERAL INFORMATION:
/ APPLICANT: Decristofaro, Marc
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Miller, Charles
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Zhong, Mei
/ APPLICANT: Anderson, David
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Rattelli, Luca
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Zernhusen, Bryan
```

```
/ APPLICANT: Andrew, David
/ APPLICANT: Mezeb, Peter
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Eissen, Andrew
/ APPLICANT: Wolenc, Adam
/ APPLICANT: Baumgartner, Jason
/ APPLICANT: Shinkete, Richard
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Vernet, Corine
/ APPLICANT: Taupier Jr., Raymond
/ APPLICANT: Pena, Carol
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Li, Li
/ APPLICANT: Casman, Stacie
/ APPLICANT: Boldog, Ferenc
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
/ FILE REFERENCE: 21402-251
/ CURRENT APPLICATION NUMBER: US/10/055,877
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,598
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/263,799
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/264,117
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,139
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ PRIOR FILING DATE: 2001-03-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 207
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-055-877-207

Query Match          52.7%; Score 545.5; DB 6; Length 189;
Best Local Similarity 55.1%; Pred. No. 9.1e-52;
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;
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/ Publication No. US20050288241A1
/ GENERAL INFORMATION:
/ APPLICANT: Decristofaro, Marc
/ APPLICANT: Padigar, Muraidhara
/ APPLICANT: Miller, Charles
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Zhong, Mei
/ APPLICANT: Anderson, David
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Ratelli, Luca
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Zernhusen, Bryan
/ APPLICANT: Andrew, David
/ APPLICANT: Mezeb, Peter
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Eissen, Andrew
/ APPLICANT: Wolenc, Adam
/ APPLICANT: Baumgartner, Jason
/ APPLICANT: Shinkete, Richard
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Vernet, Corine
/ APPLICANT: Taupier Jr., Raymond
/ APPLICANT: Pena, Carol
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Li, Li
/ APPLICANT: Casman, Stacie
/ APPLICANT: Boldog, Ferenc
/ TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
/ FILE REFERENCE: 21402-251
/ CURRENT APPLICATION NUMBER: US/10/055,877
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,598
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/263,799
/ PRIOR FILING DATE: 2001-01-24
/ PRIOR APPLICATION NUMBER: 60/264,117
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,139
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/264,478
/ PRIOR FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/263,351
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/272,870
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/275,990
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/275,927
/ PRIOR FILING DATE: 2001-03-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 512
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 209
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-055-877-209

Query Match          50.7%; Score 525.5; DB 6; Length 189;
Best Local Similarity 53.5%; Pred. No. 1.3e-49;
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;
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Db 61 CGSNVSTCASCPCSDRMKRYGNHCYFVSVEKDMNSSLFECLARDSHLVTITNOEWS 120
QY 121 LFEQVEGEFFYVIGLRDIDGMRWEDGPAISLS-IISNSVQKCGTTHRCGHLASSCEVAL 179
Db 121 LQVSLSEAFMWIGLRNNSGMRWEDGSPLNFSRISNSFVQTCALINXGLQASSCEVAL 180
QY 180 GWICEKV 186
Db 181 HGVCCKV 187

RESULT 5
US-10-467-657-246
Sequence 246, Application US/10467657
Publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 246
LENGTH: 189
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-246

Query Match 4.3%; Score 45; DB 6; Length 189;
Best Local Similarity 24.6%; Pred. No. 5.9e+02;
Matches 16; Conservative 8; Mismatches 23; Indels 18; Gaps 4;

QY 113 PPDNGVNLFOEYVGEDFWIG-----LRIDGMRWEDGPAISLSIISNSVQKCGTTH 166
Db 98 YPTN---NILDIFGARLWIPSETVAGILEKLDGKTEY-----LKNWYLRDAGGY- 146
QY 167 RCGHL 171
Db 147 -IGIH 150

RESULT 6
US-10-467-657-2690
Sequence 2690, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 2690
LENGTH: 189
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2690

Query Match 4.3%; Score 45; DB 6; Length 189;
Best Local Similarity 24.6%; Pred. No. 5.9e+02;
Matches 16; Conservative 8; Mismatches 23; Indels 18; Gaps 4;
QY 113 PPDNGVNLFOEYVGEDFWIG-----LRIDGMRWEDGPAISLSIISNSVQKCGTTH 166
Db 98 YPTN---NILDIFGARLWIPSETVAGILEKLDGKTEY-----LKNWYLRDAGGY- 146
QY 167 RCGHL 171
Db 147 -IGIH 150

RESULT 7
US-10-131-826A-240
Sequence 240, Application US/10131826A
Publication No. US20050245730A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 240
LENGTH: 189
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-240

Query Match 4.3%; Score 44.5; DB 6; Length 189;
Best Local Similarity 20.1%; Pred. No. 6.6e+02;
Matches 37; Conservative 25; Mismatches 47; Indels 75; Gaps 11;
QY 28 AVLRPCVSLVWVALGLTVITLMSLLYORTLCCGSKGFMCSCCSCRCPNLMRNGSHCY 87

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Db      2 ALLSRP-----ALTTLLLLMAAIV-----RCGE-----24
Qy      88 YESMEKRDVNSLKKCADKSHLTFEPDNOGVNLFQEVGDFPVMGL---RDIDG-----140
Db      25 --QAOTTBRAATLKTRN-GVKIKIDTYLMAALDLG---GED---GLCQYKCSDSKPF 74
Qy      141 --WRWEDGPA-----LSLSILSNSVYQKCTIHRCG-----RCGLHASSCEVALQNI 182
Db      75 PRYGVKSPSPNGCGSPLFCVHNLIGIPG---LTRCNQNDRCVETCGKSKNDCEBFQYC 131
Qy      183 CEKV 186
Db      132 LSKI 135

RESULT 8
US-10-945-853-2
; Sequence 2, Application US/10945853
; Publication No. US20050255117A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Sanicola-Nadel, Michele
; APPLICANT: Adkins, Heather
; APPLICANT: Miklasz, Steven Donald
; APPLICANT: Rayhorn, Paul
; APPLICANT: Schiffer, Susan Gail
; APPLICANT: Williams, Kevin
; TITLE OF INVENTION: CripTo-Specific Antibodies
; FILE REFERENCE: BGNAL17CPCCN
; CURRENT APPLICATION NUMBER: US/10/945,853
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: PCT/US02/31462
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: PCT/US02/11950
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/286,782
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/293,020
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/301,091
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/367,002
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-945-853-2

Query Match      4.1%; Score 42.5; DB 6; Length 188;
Best Local Similarity 27.9%; Pred. No. 1.1e+03;
Matches 19; Conservative 8; Mismatches 34; Indels 7; Gaps 2;

Qy      19 QDDSRMKVKAHIVPCVSYLVWVALGLTIVILMSLLYQRTLC--GSKGFMCSQGRCPN 77
Db      47 RDSISIPQEBPARPRSSQSV-----LPMGIGHSKELNRTCTCLNGTCTMLBFCACPFS 100
Qy      78 LWMRNGSH 85
Db      101 FYGRNCEH 108

RESULT 9
US-11-064-774A-117
; Sequence 117, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Alltalo et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWT
; FILE REFERENCE: 28967/35977B2
```

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; CURRENT APPLICATION NUMBER: US/11/064,774A
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-774A-117

Query Match      4.0%; Score 41; DB 7; Length 188;
Best Local Similarity 31.6%; Pred. No. 1.6e+03;
Matches 6; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy      151 LSILSNSVYQKCTIHRCG 169
Db      61 MGTVAKQLVPSCVTVQRCG 79

RESULT 10
US-11-137-465-60
; Sequence 60, Application US/11137465
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahllick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FaSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-60

Query Match      4.0%; Score 41; DB 7; Length 189;
Best Local Similarity 35.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy      144 EDGPALSLISNSVYQKCG 163
Db      168 DDEHKMSVHYVNTSLVXKCG 187

RESULT 11
US-10-131-826A-232
; Sequence 232, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
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/ PRIOR APPLICATION NUMBER: PCT/US02/31462
/ PRIOR FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: PCT/US02/11950
/ PRIOR FILING DATE: 2002-04-17
/ PRIOR APPLICATION NUMBER: 60/286,782
/ PRIOR FILING DATE: 2001-04-26
/ PRIOR APPLICATION NUMBER: 60/293,020
/ PRIOR FILING DATE: 2001-05-17
/ PRIOR APPLICATION NUMBER: 60/301,091
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 60/367,002
/ PRIOR FILING DATE: 2002-03-22
/ NUMBER OF SEQ ID NOS: 9
/ SEQ ID NO 1
/ LENGTH: 188
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-945-853-1
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Query Match          3.8%; Score 39.5; DB 6; Length 188;
Best Local Similarity 26.4%; Pred. No. 2.2e+03;
Matches 19; Conservative 10; Mismatches 28; Indels 15; Gaps 4;
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QY 19 QDSSMKKAVLHRCVSLVWVALGLVILMSLLYQRTL---CC--GSKGFMCSQS 73
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 47 RDDSIVPQEEPAIRPRSSQRV--PPWG-----IOHSEKILRTCTCLNGTCMLGSFCA 96
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QY 74 RCPNLMRNGSH 85
   ||| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 97 CPSPFYGRNCEH 108
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RESULT 15
US-11-147-492-30
/ Sequence 30, Application US/11147492
/ Publication No. US20050276785A1
/ GENERAL INFORMATION:
/ APPLICANT: KAPP, Joachim-Freidrich
/ APPLICANT: Kuehl, Uwe
/ APPLICANT: Groetzbach, Georg
/ APPLICANT: Schulteis, Heinz-Peter
/ APPLICANT: Sowade, Olaf
/ APPLICANT: Stuerzebecher, Claus-Steffen
/ TITLE OF INVENTION: Treatment of Cardiomypopathy and Endothelial Dysfunction
/ FILE REFERENCE: 53223
/ CURRENT APPLICATION NUMBER: US/11/147,492
/ CURRENT FILING DATE: 2005-06-07
/ PRIOR APPLICATION NUMBER: US 60/579,024
/ PRIOR FILING DATE: 2004-06-04
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 30
/ LENGTH: 189
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-147-492-30
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Query Match          3.8%; Score 39.5; DB 7; Length 189;
Best Local Similarity 16.3%; Pred. No. 2.2e+03;
Matches 22; Conservative 23; Mismatches 59; Indels 31; Gaps 5;
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QY 47 TVILMSLLTYQRTL---CGSKG--FMCSCSRCPNLMRNGSHCYPSMEK 93
   ||| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 6 SLMAVIVLYKSCISGCLLPQTHSLGNRALILLQWGRISPSCCLKDRHDFGFPQEE 65
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QY 94 RDWNSSLKFCADKSHLLTPPDNGVNLFOBYGEGDFYWGIRDIDGWRWEDGPAISLST 153
   ||| | | | | | | | | | | | | | | | | | | | | | | | | |
DB 66 FDGNO-----FOKAQAIISVLEHMIQOTFNLPSTKDSQA-TWEOS---LLEK 107
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QY 154 LSNVVOKCGTIHRC 168
   ||| | | | | | | | | | | | | | | | | | | | | | | | |
DB 108 FSTELNQQLNDMEAC 122
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